SEQUENCE LISTING

<110> Takeda Chemical Industries, Ltd.

<120> Novel G Protein Coupled Receptor Protein and Its Use

<130> A99137

<150> JP 10-207579

<151> 1998-07-23

<150> JP 10-225060

<151> 1998-08-07

<150> JP 10-284328

<151> 1998-10-06

<160> 6

<210> 1

<211> 872

<212> PRT

<213> Human

<400> 1

Ala Glu Gln Thr Arg Asn His Leu Asn Ala Gly Asp Ile Thr Tyr Ser
1   5   10   15

Val Arg Ala Met Asp Gln Leu Val Gly Leu Leu Asp Val Gln Leu Arg
                20   25   30

86

Asn Leu Thr Pro Gly Gly Lys Asp Ser Ala Ala Arg Ser Leu Asn Lys

       35   40   45

Ala Met Val Glu Thr Val Asn Asn Leu Leu Gln Pro Gln Ala Leu Asn

       50   55   60

5   Ala Trp Arg Asp Leu Thr Thr Ser Asp Gln Leu Arg Ala Ala Thr Met

   65   70   75   80

Leu Leu His Thr Val Glu Glu Ser Ala Phe Val Leu Ala Asp Asn Leu

            85   90   95

Leu Lys Thr Asp Ile Val Arg Glu Asn Thr Asp Asn Ile Lys Leu Glu

10   100   105   110

Val Ala Arg Leu Ser Thr Glu Gly Asn Leu Glu Asp Leu Lys Phe Pro

       115   120   125

Glu Asn Met Gly His Gly Ser Thr Ile Gln Leu Ser Ala Asn Thr Leu

       130   135   140

15 Lys Gln Asn Gly Arg Asn Gly Glu Ile Arg Val Ala Phe Val Leu Tyr

145   150   155   160

Asn Asn Leu Gly Pro Tyr Leu Ser Thr Glu Asn Ala Ser Met Lys Leu

       165   170   175

Gly Thr Glu Ala Leu Ser Thr Asn His Ser Val Ile Val Asn Ser Pro

20   180   185   190

Val Ile Thr Ala Ala Ile Asn Lys Glu Phe Ser Asn Lys Val Tyr Leu

       195   200   205

Ala Asp Pro Val Val Phe Thr Val Lys His Ile Lys Gln Ser Glu Glu

       210   215   220

25 Asn Phe Asn Pro Asn Cys Ser Phe Trp Ser Tyr Ser Lys Arg Thr Met

```
              225                 230                 235                 240

          Thr Gly Tyr Trp Ser Thr Gln Gly Cys Arg Leu Leu Thr Thr Asn Lys
                          245                 250                 255

          Thr His Thr Thr Cys Ser Cys Asn His Leu Thr Asn Phe Ala Val Leu
     5                    260                 265                · 270·

          Met Ala His Val Glu Val Lys His Ser Asp Ala Val His Asp Leu Leu
                      275                 280                 285

          Leu Asp Val Ile Thr Trp Val Gly Ile Leu Leu Ser Leu Val Cys Leu
                      290                 295                 300

     10   Leu Ile Cys Ile Phe Thr Phe Cys Phe Phe Arg Gly Leu Gln Ser Asp
          305                 310                 315                 320

          Arg Asn Thr Ile His Lys Asn Leu Cys Ile Ser Leu Phe Val Ala Glu
                          325                 330                 335

          Leu Leu Phe Leu Ile Gly Ile Asn Arg Thr Asp Gln Pro Ile Ala Cys
     15                   340                 345                 350

          Ala Val Phe Ala Ala Leu Leu His Phe Phe Phe Leu Ala Ala Phe Thr
                      355                 360                 365

          Trp Met Phe Leu Glu Gly Val Gln Leu Tyr Ile Met Leu Val Glu Val
                      370                 375                 380

     20   Phe Glu Ser Glu His Ser Arg Arg Lys Tyr Phe Tyr Leu Val Gly Tyr
          385                 390                 395                 400

          Gly Met Pro Ala Leu Ile Val Ala Val Ser Ala Ala Val Asp Tyr Arg
                          405                 410                 415

          Ser Tyr Gly Thr Asp Lys Val Cys Trp Leu Arg Leu Asp Thr Tyr Phe
     25                   420                 425                 430

                                         88
```

Ile Trp Ser Phe Ile Gly Pro Ala Thr Leu Ile Ile Met Leu Asn Val

435   440   445

Ile Phe Leu Gly Ile Ala Leu Tyr Lys Met Phe His His Thr Ala Ile

450   455   460

5 Leu Lys Pro Glu Ser Gly Cys Leu Asp Asn Ile Lys Ser Trp Val Ile

465   470   475   480

Gly Ala Ile Ala Leu Leu Cys Leu Leu Gly Leu Thr Trp Ala Phe Gly

485   490   495

Leu Met Tyr Ile Asn Glu Ser Thr Val Ile Met Ala Tyr Leu Phe Thr

10   500   505   510

Ile Phe Asn Ser Leu Gln Gly Met Phe Ile Phe Ile Phe His Cys Val

515   520   525

Leu Gln Lys Lys Val Arg Lys Glu Tyr Gly Lys Cys Leu Arg Thr His

530   535   540

15 Cys Cys Ser Gly Lys Ser Thr Glu Ser Ser Ile Gly Ser Gly Lys Thr

545   550   555   560

Ser Gly Ser Arg Thr Pro Gly Arg Tyr Ser Thr Gly Ser Gln Ser Arg

565   570   575

Ile Arg Arg Met Trp Asn Asp Thr Val Arg Lys Gln Ser Glu Ser Ser

20   580   585   590

Phe Ile Thr Gly Asp Ile Asn Ser Ser Ala Ser Leu Asn Arg Glu Gly

595   600   605

Leu Leu Asn Asn Ala Arg Asp Thr Ser Val Met Asp Thr Leu Pro Leu

610   615   620

25 Asn Gly Asn His Gly Asn Ser Tyr Ser Ile Ala Ser Gly Glu Tyr Leu

89

```
                625                630                635                640

        Ser Asn Cys Val Gln Ile Ile Asp Arg Gly Tyr Asn His Asn Glu Thr
                        645                650                655

        Ala Leu Glu Lys Lys Ile Leu Lys Glu Leu Thr Ser Asn Tyr Ile Pro
    5                   660                665                670

        Ser Tyr Leu Asn Asn His Glu Arg Ser Ser Glu Gln Asn Arg Asn Leu
                    675                680                685

        Met Asn Lys Leu Val Asn Asn Leu Gly Ser Gly Arg Glu Asp Asp Ala
                    690                695                700

    10  Ile Val Leu Asp Asp Ala Thr Ser Phe Asn His Glu Glu Ser Leu Gly
        705                710                715                720

        Leu Glu Leu Ile His Glu Glu Ser Asp Ala Pro Leu Leu Pro Pro Arg
                        725                730                735

        Val Tyr Ser Thr Glu Asn His Gln Pro His His Tyr Thr Arg Arg Arg
    15                  740                745                750

        Ile Pro Gln Asp His Ser Glu Ser Phe Phe Pro Leu Leu Thr Asn Glu
                    755                760                765

        His Thr Glu Asp Leu Gln Ser Pro His Arg Asp Ser Leu Tyr Thr Ser
                    770                775                780

    20  Met Pro Thr Leu Ala Gly Val Ala Ala Thr Glu Ser Val Thr Thr Ser
        785                790                795                800

        Thr Gln Thr Glu Pro Pro Pro Ala Lys Cys Gly Asp Ala Glu Asp Val
                        805                810                815

        Tyr Tyr Lys Ser Met Pro Asn Leu Gly Ser Arg Asn His Val His Gln
    25                  820                825                830

                                    90
```

Leu His Thr Tyr Tyr Gln Leu Gly Arg Gly Ser Ser Asp Gly Phe Ile

     835   840   845

Val Pro Pro Asn Lys Asp Gly Thr Pro Pro Glu Gly Ser Ser Lys Gly

     850   855   860

Pro Ala His Leu Val Thr Ser Leu

865   870

<210> 2

<211> 2616

<212> DNA

<213> Human

<400> 2

GCTGAACAGA CAAGAAATCA CTTGAATGCT GGGGACATCA CCTACTCTGT CCGGGCCATG   60

GACCAGCTGG TAGGCCTCCT AGATGTACAG CTTCGGAACT TGACCCCAGG TGGAAAAGAT   120

AGTGCTGCCC GGAGTTTGAA CAAGGCAATG GTCGAGACAG TTAACAACCT CCTTCAGCCA   180

CAAGCTTTGA ATGCATGGAG AGACCTGACT ACGAGTGATC AGCTGCGTGC GGCCACCATG   240

TTGCTTCATA CTGTGGAGGA AAGTGCTTTT GTGCTGGCTG ATAACCTTTT GAAGACTGAC   300

ATTGTCAGGG AGAATACAGA CAATATTAAA TTGGAAGTTG CAAGACTGAG CACAGAAGGA   360

AACTTAGAAG ACCTAAAATT TCCAGAAAAC ATGGGCCATG GAAGCACTAT CCAGCTGTCT   420

GCAAATACCT TAAAGCAAAA TGGCCGAAAT GGAGAGATCA GAGTGGCCTT TGTCCTGTAT   480

AACAACTTGG GTCCTTATTT ATCCACGGAG AATGCCAGTA TGAAGTTGGG AACGGAAGCT   540

TTGTCCACAA ATCATTCTGT TATTGTCAAT TCCCCTGTTA TTACGGCAGC AATAAACAAA   600

GAGTTCAGTA ACAAGGTTTA TTTGGCTGAT CCTGTGGTAT TTACTGTTAA ACATATCAAG   660

CAGTCAGAGG AAAATTTCAA CCCTAACTGT TCATTTTGGA GCTACTCCAA GCGTACAATG   720

ACAGGTTATT GGTCAACACA AGGCTGTCGG CTCCTGACAA CAAATAAGAC ACATACTACA   780

TGCTCTTGTA ACCACCTAAC AAATTTTGCA GTACTGATGG CACATGTGGA AGTTAAGCAC   840

91

92

CTCTATACCA GCATGCCGAC ACTGGCTGGT GTGGCCGCCA CAGAGAGTGT TACCACCAGC 2400

ACCCAGACCG AACCCCCACC GGCCAAATGT GGTGATGCCG AAGATGTTTA CTACAAAAGC 2460

ATGCCAAACC TAGGCTCCAG AAACCACGTC CATCAGCTGC ATACTTACTA CCAGCTAGGT 2520

CGCGGCAGCA GTGATGGATT TATAGTTCCT CCAAACAAAG ATGGGACCCC TCCCGAGGGA 2580

AGTTCAAAAG GACCGGCTCA TTTGGTCACT AGTCTA 2616

<210> 3

<211> 1021

<212> PRT

<213> Human

<400> 3

Glu Gly Ser Lys Gly Thr Lys Pro Pro Pro Ala Val Ser Thr Thr Lys
1   5   10   15

Ile Pro Pro Ile Thr Asn Ile Phe Pro Leu Pro Glu Arg Phe Cys Glu
            20   25   30

Ala Leu Asp Ser Lys Gly Ile Lys Trp Pro Gln Thr Gln Arg Gly Met
        35   40   45

Met Val Glu Arg Pro Cys Pro Lys Gly Thr Arg Gly Thr Ala Ser Tyr
        50   55   60

Leu Cys Met Ile Ser Thr Gly Thr Trp Asn Pro Lys Gly Pro Asp Leu
65   70   75   80

Ser Asn Cys Thr Ser His Trp Val Asn Gln Leu Ala Gln Lys Ile Arg
                85   90   95

Ser Gly Glu Asn Ala Ala Ser Leu Ala Asn Glu Leu Ala Lys His Thr
            100   105   110

Lys Gly Pro Val Phe Ala Gly Asp Val Ser Ser Ser Val Arg Leu Met

                115   120   125

Glu Gln Leu Val Asp Ile Leu Asp Ala Gln Leu Gln Glu Leu Lys Pro

            130   135   140

Ser Glu Lys Asp Ser Ala Gly Arg Ser Tyr Asn Lys Leu Gln Lys Arg

5   145   150   155   160

Glu Lys Thr Cys Arg Ala Tyr Leu Lys Ala Ile Val Asp Thr Val Asp

                    165   170   175

Asn Leu Leu Arg Pro Glu Ala Leu Glu Ser Trp Lys His Met Asn Ser

                    180   185   190

10 Ser Glu Gln Ala His Thr Ala Thr Met Leu Leu Asp Thr Leu Glu Glu

                195   200   205

Gly Ala Phe Val Leu Ala Asp Asn Leu Leu Glu Pro Thr Arg Val Ser

            210   215   220

Met Pro Thr Glu Asn Ile Val Leu Glu Val Ala Val Leu Ser Thr Glu

15 225   230   235   240

Gly Gln Ile Gln Asp Phe Lys Phe Pro Leu Gly Ile Lys Gly Ala Gly

                    245   250   255

Ser Ser Ile Gln Leu Ser Ala Asn Thr Val Lys Gln Asn Ser Arg Asn

                260   265   270

20 Gly Leu Ala Lys Leu Val Phe Ile Ile Tyr Arg Ser Leu Gly Gln Phe

                275   280   285

Leu Ser Thr Glu Asn Ala Thr Ile Lys Leu Gly Ala Asp Phe Ile Gly

                290   295   300

Arg Asn Ser Thr Ile Ala Val Asn Ser His Val Ile Ser Val Ser Ile

25 305   310   315   320

Asn Lys Glu Ser Ser Arg Val Tyr Leu Thr Asp Pro Val Leu Phe Thr
                325   330   335

Leu Pro His Ile Asp Pro Asp Asn Tyr Phe Asn Ala Asn Cys Ser Phe
                340   345   350

5   Trp Asn Tyr Ser Glu Arg Thr Met Met Gly Tyr Trp Ser Thr Gln Gly
                355   360   365

Cys Lys Leu Val Asp Thr Asn Lys Thr Arg Thr Thr Cys Ala Cys Ser
                370   375   380

His Leu Thr Asn Phe Ala Ile Leu Met Ala His Arg Glu Ile Ala Tyr
10 385   390   395   400

Lys Asp Gly Val His Glu Leu Leu Leu Thr Val Ile Thr Trp Val Gly
                405   410   415

Ile Val Ile Ser Leu Val Cys Leu Ala Ile Cys Ile Phe Thr Phe Cys
                420   425   430

15 Phe Phe Arg Gly Leu Gln Ser Asp Arg Asn Thr Ile His Lys Asn Leu
                435   440   445

Cys Ile Asn Leu Phe Ile Ala Glu Phe Ile Phe Leu Ile Gly Ile Asp
                450   455   460

Lys Thr Lys Tyr Ala Ile Ala Cys Pro Ile Phe Ala Gly Leu Leu His
20 465   470   475   480

Phe Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Leu Glu Gly Val Gln
                485   490   495

Leu Tyr Leu Met Leu Val Glu Val Phe Glu Ser Glu Tyr Ser Arg Lys
                500   505   510

25 Lys Tyr Tyr Tyr Val Ala Gly Tyr Leu Phe Pro Ala Thr Val Val Gly

```
                515                 520                 525
        Val Ser Ala Ala Ile Asp Tyr Lys Ser Tyr Gly Thr Glu Lys Ala Cys
                530                 535                 540
        Trp Leu His Val Asp Asn Tyr Phe Ile Trp Ser Phe Ile Gly Pro Val
   5    545                 550                 555                 560
        Thr Phe Ile Ile Leu Leu Asn Ile Ile Phe Leu Val Ile Thr Leu Cys
                        565                 570                 575
        Lys Met Val Lys His Ser Asn Thr Leu Lys Pro Asp Ser Ser Arg Leu
                        580                 585                 590
  10    Glu Asn Ile Lys Ser Trp Val Leu Gly Ala Phe Ala Leu Leu Cys Leu
                        595                 600                 605
        Leu Gly Leu Thr Trp Ser Phe Gly Leu Leu Phe Ile Asn Glu Glu Thr
                        610                 615                 620
        Ile Val Met Ala Tyr Leu Phe Thr Ile Phe Asn Ala Phe Gln Gly Val
  15    625                 630                 635                 640
        Phe Ile Phe Ile Phe His Cys Ala Leu Gln Lys Lys Val Arg Lys Glu
                        645                 650                 655
        Tyr Gly Lys Cys Phe Arg His Ser Tyr Cys Cys Gly Gly Leu Pro Thr
                        660                 665                 670
  20    Glu Ser Pro His Ser Ser Val Lys Ala Ser Thr Thr Arg Thr Ser Ala
                        675                 680                 685
        Arg Tyr Ser Ser Gly Thr Gln Ser Arg Ile Arg Arg Met Trp Asn Asp
                690                 695                 700
        Thr Val Arg Lys Gln Ser Glu Ser Ser Phe Ile Ser Gly Asp Ile Asn
  25    705                 710                 715                 720
```

96

Ser Thr Ser Thr Leu Asn Gln Gly Met Thr Gly Asn Tyr Leu Leu Thr

          725   730   735

Asn Pro Leu Leu Arg Pro His Gly Thr Asn Asn Pro Tyr Asn Thr Leu

          740   745   750

5   Leu Ala Glu Thr Val Val Cys Asn Ala Pro Ser Ala Pro Val Phe Asn

          755   760   · 765

Ser Pro Gly His Ser Leu Asn Asn Ala Arg Asp Thr Ser Ala Met Asp

          770   775   780

Thr Leu Pro Leu Asn Gly Asn Phe Asn Asn Ser Tyr Ser Leu His Lys

10 785   790   795   800

Gly Asp Tyr Asn Asp Ser Val Gln Val Val Asp Cys Gly Leu Ser Leu

             805   810   815

Asn Asp Thr Ala Phe Glu Lys Met Ile Ile Ser Glu Leu Val His Asn

          820   825   830

15 Asn Leu Arg Gly Ser Ser Lys Thr His Asn Leu Glu Leu Thr Leu Pro

            835   840   845

Val Lys Pro Val Ile Gly Gly Ser Ser Ser Glu Asp Asp Ala Ile Val

          850   855   860

Ala Asp Ala Ser Ser Leu Met His Ser Asp Asn Pro Gly Leu Glu Leu

20 865   870   875   880

His His Lys Glu Leu Glu Ala Pro Leu Ile Pro Gln Arg Thr His Ser

            885   890   895

Leu Leu Tyr Gln Pro Gln Lys Lys Val Lys Ser Glu Gly Thr Asp Ser

          900   905   910

25 Tyr Val Ser Gln Leu Thr Ala Glu Ala Glu Asp His Leu Gln Ser Pro

97

Asn Arg Asp Ser Leu Tyr Thr Ser Met Pro Asn Leu Arg Asp Ser Pro

        930   935   940

Tyr Pro Glu Ser Ser Pro Asp Met Glu Glu Asp Leu Ser Pro Ser Arg

945   950   955   960

Arg Ser Glu Asn Glu Asp Ile Tyr Tyr Lys Ser Met Pro Asn Leu Gly

                965   970   975

Ala Gly His Gln Leu Gln Met Cys Tyr Gln Ile Ser Arg Gly Asn Ser

                980   985   990

Asp Gly Tyr Ile Ile Pro Ile Asn Lys Glu Gly Cys Ile Pro Glu Gly

        995   1000   1005

Asp Val Arg Glu Gly Gln Met Gln Leu Val Thr Ser Leu

        1010   1015   1020

<210> 4

<211> 3063

<212> DNA

<213> Human

<400> 4

GAAGGAAGCA AAGGGACAAA ACCACCTCCA GCAGTTTCTA CAACCAAAAT TCCACCTATA   60

ACAAATATTT TTCCCCTGCC AGAGAGATTC TGTGAAGCAT TAGACTCCAA GGGGATAAAG   120

TGGCCTCAGA CACAAAGGGG AATGATGGTT GAACGACCAT GCCCTAAGGG AACAAGAGGA   180

ACTGCCTCAT ATCTCTGCAT GATTTCCACT GGAACATGGA ACCCTAAGGG CCCCGATCTT   240

AGCAACTGTA CCTCACACTG GGTGAATCAG CTGGCTCAGA AGATCAGAAG CGGAGAAAAT   300

GCTGCTAGTC TTGCCAATGA ACTGGCTAAA CATACCAAAG GGCCAGTGTT TGCTGGGGAT   360

GTAAGTTCTT CAGTGAGATT GATGGAGCAG TTGGTGGACA TCCTTGATGC ACAGCTGCAG   420

```
GAACTGAAAC CTAGTGAAAA AGATTCAGCT GGACGGAGTT ATAACAAGCT CCAAAAACGA  480

GAGAAGACAT GCAGGGCTTA CCTTAAGGCA ATTGTTGACA CAGTGGACAA CCTTCTGAGA  540

CCTGAAGCTT TGGAATCATG GAAACATATG AATTCTTCTG AACAAGCACA TACTGCAACA  600

ATGTTACTCG ATACATTGGA AGAAGGAGCT TTTGTCCTAG CTGACAATCT TTTAGAACCA  660

ACAAGGGTCT CAATGCCCAC AGAAAATATT GTCCTGGAAG TTGCCGTACT CAGTACAGAA  720

GGACAGATCC AAGACTTTAA ATTTCCTCTG GGCATCAAAG GAGCAGGCAG CTCAATCCAA  780

CTGTCCGCAA ATACCGTCAA ACAGAACAGC AGGAATGGGC TTGCAAAGTT GGTGTTCATC  840

ATTTACCGGA GCCTGGGACA GTTCCTTAGT ACAGAAAATG CAACCATTAA ACTGGGTGCT  900

GATTTTATTG GTCGTAATAG CACCATTGCA GTGAACTCTC ACGTCATTTC AGTTTCAATC  960

AATAAAGAGT CCAGCCGAGT ATACCTGACT GATCCTGTGC TTTTTACCCT GCCACACATT 1020

GATCCTGACA ATTATTTCAA TGCAAACTGC TCCTTCTGGA ACTACTCAGA GAGAACTATG 1080

ATGGGATATT GGTCTACCCA GGGCTGCAAG CTGGTTGACA CTAATAAAAC TCGAACAACG 1140

TGTGCATGCA GCCACCTAAC CAATTTTGCA ATTCTCATGG CCCACAGGGA AATTGCATAT 1200

AAAGATGGCG TTCATGAATT ACTTCTTACA GTCATCACCT GGGTGGGAAT TGTCATTTCC 1260

CTTGTTTGCC TGGCTATCTG CATCTTCACC TTCTGCTTTT TCCGTGGCCT ACAGAGTGAC 1320

CGAAATACTA TTCACAAGAA CCTTTGTATC AACCTTTTCA TTGCTGAATT TATTTTCCTA 1380

ATAGGCATTG ATAAGACAAA ATATGCGATT GCATGCCCAA TATTTGCAGG ACTTCTACAC 1440

TTTTTCTTTT TGGCAGCTTT TGCTTGGATG TGCCTAGAAG GTGTGCAGCT CTACCTAATG 1500

TTAGTTGAAG TTTTTGAAAG TGAATATTCA AGGAAAAAAT ATTACTATGT TGCTGGTTAC 1560

TTGTTTCCTG CCACAGTGGT TGGAGTTTCA GCTGCTATTG ACTATAAGAG CTATGGAACA 1620

GAAAAAGCTT GCTGGCTTCA TGTTGATAAC TACTTTATAT GGAGCTTCAT TGGACCTGTT 1680

ACCTTCATTA TTCTGCTAAA TATTATCTTC TTGGTGATCA CATTGTGCAA AATGGTGAAG 1740

CATTCAAACA CTTTGAAACC AGATTCTAGC AGGTTGGAAA ACATTAAGTC TTGGGTGCTT 1800

GGCGCTTTCG CTCTTCTGTG TCTTCTTGGC CTCACCTGGT CCTTTGGGTT GCTTTTTATT 1860

AATGAGGAGA CTATTGTGAT GGCATATCTC TTCACTATAT TTAATGCTTT CCAGGGAGTG 1920
```

99

TTCATTTTCA TCTTTCACTG TGCTCTCCAA AAGAAAGTAC GAAAAGAATA TGGCAAGTGC 1980

TTCAGACACT CATACTGCTG TGGAGGCCTC CCAACTGAGA GTCCCCACAG TTCAGTGAAG 2040

GCATCAACCA CCAGAACCAG TGCTCGCTAT TCCTCTGGCA CACAGAGTCG TATAAGAAGA 2100

ATGTGGAATG ATACTGTGAG AAAACAATCA GAATCTTCTT TTATCTCAGG TGACATCAAT 2160

AGCACTTCAA CACTTAATCA AGGAATGACT GGCAATTACC TACTAACAAA CCCTCTTCTT 2220

CGACCCCACG GCACTAACAA CCCCTATAAC ACATTGCTCG CTGAAACAGT TGTATGTAAT 2280

GCCCCTTCAG CTCCTGTATT TAACTCACCA GGACATTCAC TGAACAATGC CAGGGATACA 2340

AGTGCCATGG ATACTCTACC GCTAAATGGT AATTTTAACA ACAGCTACTC GCTGCACAAG 2400

GGTGACTATA ATGACAGCGT GCAAGTTGTG GACTGTGGAC TAAGTCTGAA TGATACTGCT 2460

TTTGAGAAAA TGATCATTTC AGAATTAGTG CACAACAACT TACGGGGCAG CAGCAAGACT 2520

CACAACCTCG AGCTCACGCT ACCAGTCAAA CCTGTGATTG GAGGTAGCAG CAGTGAAGAT 2580

GATGCTATTG TGGCAGATGC TTCATCTTTA ATGCACAGCG ACAACCCAGG GCTGGAGCTC 2640

CATCACAAAG AACTCGAGGC ACCACTTATT CCTCAGCGGA CTCACTCCCT TCTGTACCAA 2700

CCCCAGAAGA AAGTGAAGTC CGAGGGAACT GACAGCTATG TCTCCCAACT GACAGCAGAG 2760

GCTGAAGATC ACCTACAGTC CCCCAACAGA GACTCTCTTT ATACAAGCAT GCCCAATCTT 2820

AGAGACTCTC CCTATCCGGA GAGCAGCCCT GACATGGAAG AAGACCTCTC TCCCTCCAGG 2880

AGGAGTGAGA ATGAGGACAT TTACTATAAA AGCATGCCAA ATCTTGGAGC TGGCCATCAG 2940

CTTCAGATGT GCTACCAGAT CAGCAGGGGC AATAGTGATG GTTATATAAT CCCCATTAAC 3000

AAAGAAGGGT GTATTCCAGA AGGAGATGTT AGAGAAGGAC AAATGCAGCT GGTTACAAG 3060

CTT   3063

<210> 5

<211> 1474

<212> PRT

<213> Human

<400> 5

Met Ala Arg Leu Ala Ala Val Leu Trp Asn Leu Cys Val Thr Ala Val
                5   10   15

Leu Val Thr Ser Ala Thr Gln Gly Leu Ser Arg Ala Gly Leu Pro Phe
                20   25   30

5   Gly Leu Met Arg Arg Glu Leu Ala Cys Glu Gly Tyr Pro Ile Glu Leu
                   35   40   45

Arg Cys Pro Gly Ser Asp Val Ile Met Val Glu Asn Ala Asn Tyr Gly
                   50   55   60

Arg Thr Asp Asp Lys Ile Cys Asp Ala Asp Pro Phe Gln Met Glu Asn
10   65   70   75   80

Val Gln Cys Tyr Leu Pro Asp Ala Phe Lys Ile Met Ser Gln Arg Cys
                            85   90   95

Asn Asn Arg Thr Gln Cys Val Val Val Ala Gly Ser Asp Ala Phe Pro
                            100   105   110

15   Asp Pro Cys Pro Gly Thr Tyr Lys Tyr Leu Glu Val Gln Tyr Asp Cys
                            115   120   125

Val Pro Tyr Lys Val Glu Gln Lys Val Phe Val Cys Pro Gly Thr Leu
                            130   135   140

Gln Lys Val Leu Glu Pro Thr Ser Thr His Glu Ser Glu His Gln Ser
20   145   150   155   160

Gly Ala Trp Cys Lys Asp Pro Leu Gln Ala Gly Asp Arg Ile Tyr Val
                            165   170   175

Met Pro Trp Ile Pro Tyr Arg Thr Asp Thr Leu Thr Glu Tyr Ala Ser
                            180   185   190

25   Trp Glu Asp Tyr Val Ala Ala Arg His Thr Thr Thr Tyr Arg Leu Pro

101

```
                 195                    200                    205

        Asn Arg Val Asp Gly Thr Gly Phe Val Val Tyr Asp Gly Ala Val Phe

            210                    215                    220

        Tyr Asn Lys Glu Arg Thr Arg Asn Ile Val Lys Tyr Asp Leu Arg Thr

  5     225                    230                    235                240

        Arg Ile Lys Ser Gly Glu Thr Val Ile Asn Thr Ala Asn Tyr His Asp

                        245                    250                    255

        Thr Ser Pro Tyr Arg Trp Gly Gly Lys Thr Asp Ile Asp Leu Ala Val

                        260                    265                    270

 10     Asp Glu Asn Gly Leu Trp Val Ile Tyr Ala Thr Glu Gly Asn Asn Gly

                        275                    280                    285

        Arg Leu Val Val Ser Gln Leu Asn Pro Tyr Thr Leu Arg Phe Glu Gly

                    290                    295                    300

        Thr Trp Glu Thr Gly Tyr Asp Lys Arg Ser Ala Ser Asn Ala Phe Met

 15     305                    310                    315                320

        Val Cys Gly Val Leu Tyr Val Leu Arg Ser Val Tyr Val Asp Asp Asp

                        325                    330                    335

        Ser Glu Ala Ala Gly Asn Arg Val Asp Tyr Ala Phe Asn Thr Asn Ala

                    340                    345                    350

 20     Asn Arg Glu Glu Pro Val Ser Leu Thr Phe Pro Asn Pro Tyr Gln Phe

                    355                    360                    365

        Ile Ser Ser Val Asp Tyr Asn Pro Arg Asp Asn Gln Leu Tyr Val Trp

                    370                    375                    380

        Asn Asn Tyr Phe Val Val Arg Tyr Ser Leu Glu Phe Gly Pro Pro Asp

 25     385                    390                    395                400
```

102

Pro Ser Ala Gly Pro Ala Thr Ser Pro Pro Leu Ser Thr Thr Thr Thr

405 410 415

Ala Arg Pro Thr Pro Leu Thr Ser Thr Ala Ser Pro Ala Ala Thr Thr

420 425 430

5 Pro Leu Arg Arg Ala Pro Leu Thr Thr His Pro Val Gly Ala Ile Asn

435 440 445

Gln Leu Gly Pro Asp Leu Pro Pro Ala Thr Ala Pro Val Pro Ser Thr

450 455 460

Arg Arg Pro Pro Ala Pro Asn Leu His Val Ser Pro Glu Leu Phe Cys

10 465 470 475 480

Glu Pro Arg Glu Val Arg Arg Val Gln Trp Pro Ala Thr Gln Gln Gly

485 490 495

Met Leu Val Glu Arg Pro Cys Pro Lys Gly Thr Arg Gly Ile Ala Ser

500 505 510

15 Phe Gln Cys Leu Pro Ala Leu Gly Leu Trp Asn Pro Arg Gly Pro Asp

515 520 525

Leu Ser Asn Cys Thr Ser Pro Trp Val Asn Gln Val Ala Gln Lys Ile

530 535 540

Lys Ser Gly Glu Asn Ala Ala Asn Ile Ala Ser Glu Leu Ala Arg His

20 545 550 555 560

Thr Arg Gly Ser Ile Tyr Ala Gly Asp Val Ser Ser Ser Val Lys Leu

565 570 575

Met Glu Gln Leu Leu Asp Ile Leu Asp Ala Gln Leu Gln Ala Leu Arg

580 585 590

25 Pro Ile Glu Arg Glu Ser Ala Gly Lys Asn Tyr Asn Lys Met His Lys

103

                595   600   605

Arg Glu Arg Thr Cys Lys Asp Tyr Ile Lys Ala Val Val Glu Thr Val

       610   615   620

Asp Asn Leu Leu Arg Pro Glu Ala Leu Glu Ser Trp Lys Asp Met Asn

5 625   630   635   640

Ala Thr Glu Gln Val His Thr Ala Thr Met Leu Leu Asp Val Leu Glu

              645   650   655

Glu Gly Ala Phe Leu Leu Ala Asp Asn Val Arg Glu Pro Ala Arg Phe

              660   665   670

10 Leu Ala Ala Lys Glu Asn Val Val Leu Glu Val Thr Val Leu Asn Thr

       675   680   685

Glu Gly Gln Val Gln Glu Leu Val Phe Pro Gln Glu Glu Tyr Pro Arg

       690   695   700

Lys Asn Ser Ile Gln Leu Ser Ala Lys Thr Ile Lys Gln Asn Ser Arg

15 705   710   715   720

Asn Gly Val Val Lys Val Val Phe Ile Leu Tyr Asn Asn Leu Gly Leu

              725   730   735

Phe Leu Ser Thr Glu Asn Ala Thr Val Lys Leu Ala Gly Glu Ala Gly

              740   745   750

20 Pro Gly Gly Pro Gly Gly Ala Ser Leu Val Val Asn Ser Gln Val Ile

       755   760   765

Ala Ala Ser Ile Asn Lys Glu Ser Ser Arg Val Phe Leu Met Asp Pro

       770   775   780

Val Ile Phe Thr Val Ala His Leu Glu Asp Lys Asn His Phe Asn Ala

25 785   790   795   800

104

Asn Cys Ser Phe Trp Asn Tyr Ser Glu Arg Ser Met Leu Gly Tyr Trp

805   810   815

Ser Thr Gln Gly Cys Arg Leu Val Glu Ser Asn Lys Thr His Thr Thr

820   825   830

5 Cys Ala Cys Ser His Leu Thr Asn Phe Ala Val Leu Met Ala His Arg

835   840   845

Glu Ile Tyr Gln Gly Arg Ile Asn Glu Leu Leu Leu Ser Val Ile Thr

850   855   860

Trp Val Gly Ile Val Ile Ser Leu Val Cys Leu Ala Ile Cys Ile Ser

10 865   870   875   880

Thr Phe Cys Phe Leu Arg Gly Leu Gln Thr Asp Arg Asn Thr Ile His

885   890   895

Lys Asn Leu Cys Ile Asn Leu Phe Leu Ala Glu Leu Leu Phe Leu Val

900   905   910

15 Gly Ile Asp Lys Thr Gln Tyr Glu Ile Ala Cys Pro Ile Phe Ala Gly

915   920   925

Leu Leu His Tyr Phe Phe Leu Ala Ala Phe Ser Trp Leu Cys Leu Glu

930   935   940

Gly Val His Leu Tyr Leu Leu Leu Val Glu Val Phe Glu Ser Glu Tyr

20 945   950   955   960

Ser Arg Thr Lys Tyr Tyr Tyr Leu Gly Gly Tyr Cys Phe Pro Ala Leu

965   970   975

Val Val Gly Ile Ala Ala Ala Ile Asp Tyr Arg Ser Tyr Gly Thr Glu

980   985   990

25 Lys Ala Cys Trp Leu Arg Val Asp Asn Tyr Phe Ile Trp Ser Phe Ile

105

995   1000   1005

Gly Pro Val Ser Phe Val Ile Val Val Asn Leu Val Phe Leu Met Val

            1010   1015   1020

Thr Leu His Lys Met Ile Arg Ser Ser Ser Val Leu Lys Pro Asp Ser

5   1025   1030   1035   1040

Ser Arg Leu Asp Asn Ile Lys Ser Trp Ala Leu Gly Ala Ile Ala Leu

                    1045   1050   1055

Leu Phe Leu Leu Gly Leu Thr Trp Ala Phe Gly Leu Leu Phe Ile Asn

                    1060   1065   1070

10 Lys Glu Ser Val Val Met Ala Tyr Leu Phe Thr Thr Phe Asn Ala Phe

                1075   1080   1085

Gln Gly Val Phe Ile Phe Val Phe His Cys Ala Leu Gln Lys Lys Val

            1090   1095   1100

His Lys Glu Tyr Ser Lys Cys Leu Arg His Ser Tyr Cys Cys Ile Arg

15 1105   1110   1115   1120

Ser Pro Pro Gly Gly Thr His Gly Ser Leu Lys Thr Ser Ala Met Arg

                    1125   1130   1135

Ser Asn Thr Arg Tyr Tyr Thr Gly Thr Gln Ser Arg Ile Arg Arg Met

                    1140   1145   1150

20 Trp Asn Asp Thr Val Arg Lys Gln Thr Glu Ser Ser Phe Met Ala Gly

            1155   1160   1165

Asp Ile Asn Ser Thr Pro Thr Leu Asn Arg Gly Thr Met Gly Asn His

            1170   1175   1180

Leu Leu Thr Asn Pro Val Leu Gln Pro Arg Gly Gly Thr Ser Pro Tyr

25 1185   1190   1195   1200

106

Asn Thr Leu Ile Ala Glu Ser Val Gly Phe Asn Pro Ser Ser Pro Pro
          1205   1210   1215

Val Phe Asn Ser Pro Gly Ser Tyr Arg Glu Pro Lys His Pro Leu Gly
          1220   1225   1230

5   Gly Arg Glu Ala Cys Gly Met Asp Thr Leu Pro Leu Asn Gly Asn Phe
          1235   1240   1245

Asn Asn Ser Tyr Ser Leu Arg Ser Gly Asp Phe Pro Pro Gly Asp Gly
          1250   1255   1260

Gly Pro Glu Pro Pro Arg Gly Arg Asn Leu Ala Asp Ala Ala Ala Phe
10 1265   1270   1275   1280

Glu Lys Met Ile Ile Ser Glu Leu Val His Asn Asn Leu Arg Gly Ser
                1285   1290   1295

Ser Ser Ala Ala Lys Gly Pro Pro Pro Glu Pro Pro Val Pro Pro
          1300   1305   1310

15 Val Pro Gly Gly Gly Gly Glu Glu Glu Ala Gly Gly Pro Gly Gly Ala
          1315   1320   1325

Asp Arg Ala Glu Ile Glu Leu Leu Tyr Lys Ala Leu Glu Glu Pro Leu
          1330   1335   1340

Leu Leu Pro Arg Ala Gln Ser Val Leu Tyr Gln Ser Asp Leu Asp Glu
20 1345   1350   1355   1360

Ser Glu Ser Cys Thr Ala Glu Asp Gly Ala Thr Ser Arg Pro Leu Ser
                1365   1370   1375

Ser Pro Pro Gly Arg Asp Ser Leu Tyr Ala Ser Gly Ala Asn Leu Arg
          1380   1385   1390

25 Asp Ser Pro Ser Tyr Pro Asp Ser Ser Pro Glu Gly Pro Ser Glu Ala

107

                    1395   1400   1405

Leu Pro Pro Pro Pro Pro Ala Pro Pro Gly Pro Pro Glu Ile Tyr Tyr

         1410   1415   1420

Thr Ser Arg Pro Pro Ala Leu Val Ala Arg Asn Pro Leu Gln Gly Tyr

5   1425   1430   1435   1440

Tyr Gln Val Arg Arg Pro Ser His Glu Gly Tyr Leu Ala Ala Pro Gly

                 1445   1450   1455

Leu Glu Gly Pro Gly Pro Asp Gly Asp Gly Gln Met Gln Leu Val Thr

                 1460   1465   1470

10 Ser Leu

⟨210⟩ 6

⟨211⟩ 4422

⟨212⟩ DNA

⟨213⟩ Human

15 ⟨400⟩ 6

ATGGCCCGCC TAGCCGCAGT GCTCTGGAAT CTGTGTGTCA CCGCCGTCCT GGTCACCTCG 60

GCCACCCAAG GCCTGAGCCG GGCCGGGCTC CCGTTCGGGC TGATGCGCCG GGAGCTGGCG 120

TGTGAAGGCT ACCCCATCGA GCTGCGGTGC CCCGGCAGCG ACGTCATCAT GGTGGAGAAT 180

GCCAACTACG GCGCACGGA CGACAAGATT TGCGATGCTG ACCCTTTCCA GATGGAGAAT 240

20 GTGCAGTGCT ACCTGCCGGA CGCCTTCAAG ATCATGTCAC AGAGGTGTAA CAACCGCACC 300

CAGTGCGTGG TGGTCGCCGG CTCGGATGCC TTTCCTGACC CCTGTCCTGG GACCTACAAG 360

TACCTGGAGG TGCAGTACGA CTGTGTCCCC TACAAAGTGG AGCAGAAAGT CTTCGTGTGC 420

CCAGGGACCC TGCAGAAGGT GCTGGAGCCC ACCTCGACAC ACGAGTCAGA GCACCAGTCT 480

GGCGCATGGT GCAAGGACCC GCTGCAGGCG GGTGACCGCA TCTACGTGAT GCCCTGGATC 540

25 CCCTACCGCA CGGACACACT GACTGAGTAT GCCTCGTGGG AGGACTACGT GGCCGCCCGC 600

108

CACACCACCA CCTACCGCCT GCCCAACCGC GTGGATGGCA CAGGCTTTGT GGTCTACGAT 660

GGTGCCGTCT TCTACAACAA GGAGCGCACG CGCAACATCG TCAAGTATGA CCTACGGACG 720

CGCATCAAGA GCGGGGAGAC GGTCATCAAT ACCGCCAACT ACCATGACAC CTCGCCCTAC 780

CGCTGGGGCG GAAAGACCGA CATTGACCTG GCGGTGGACG AGAACGGGCT GTGGGTCATC 840

TACGCCACTG AGGGCAACAA CGGGCGGCTG GTGGTGAGCC AGCTGAACCC CTACACACTG 900

CGCTTTGAGG GCACGTGGGA GACGGGTTAC GACAAGCGCT CGGCATCCAA CGCCTTCATG 960

GTGTGTGGGG TCCTGTACGT CCTGCGCTCC GTGTACGTGG ATGATGACAG CGAGGCGGCT 1020

GGCAACCGCG TGGACTATGC CTTCAACACC AATGCCAACC GCGAGGAGCC TGTCAGCCTC 1080

ACCTTCCCCA ACCCCTACCA GTTCATCTCC TCCGTTGACT ACAACCCTCG CGACAACCAG 1140

CTGTACGTCT GGAACAACTA TTTCGTGGTG CGCTACAGCC TGGAGTTCGG GCCGCCCGAC 1200

CCCAGTGCTG GCCCAGCCAC TTCCCCACCC CTCAGCACGA CCACCACAGC CAGGCCCACG 1260

CCCCTCACCA GCACAGCCTC GCCCGCAGCC ACCACCCCGC TCCGCCGGGC ACCCCTCACC 1320

ACGCACCCAG TGGGTGCCAT CAACCAGCTG GGACCTGATC TGCCTCCAGC CACAGCCCCA 1380

GTCCCCAGCA CCCGGCGGCC CCCAGCCCCG AATCTACACG TGTCCCCTGA GCTCTTCTGC 1440

GAGCCCCGAG AGGTACGGCG GGTCCAGTGG CCGGCCACCC AGCAGGGCAT GCTGGTGGAG 1500

AGGCCCTGCC CCAAGGGGAC TCGAGGAATT GCCTCCTTCC AGTGTCTACC AGCCTTGGGG 1560

CTCTGGAACC CCCGGGGCCC TGACCTCAGC AACTGCACCT CCCCCTGGGT CAACCAGGTG 1620

GCCCAGAAGA TCAAGAGTGG GGAGAACGCG GCCAACATCG CCAGCGAGCT GGCCCGACAC 1680

ACCCGGGGCT CCATCTACGC GGGGGACGTC TCCTCCTCTG TGAAGCTGAT GGAGCAGCTG 1740

CTGGACATCC TGGATGCCCA GCTGCAGGCC CTGCGGCCCA TCGAGCGCGA GTCAGCCGGC 1800

AAGAACTACA ACAAGATGCA CAAGCGAGAG AGAACTTGTA GGATTATAT CAAGGCCGTG 1860

GTGGAGACAG TGGACAATCT GCTCCGGCCA GAAGCTCTGG AGTCCTGGAA GGACATGAAT 1920

GCCACGGAGC AGGTGCACAC GGCCACCATG CTCCTCGACG TCCTGGAGGA GGGCGCCTTC 1980

CTGCTGGCCG ACAATGTCAG GGAGCCTGCC CGCTTCCTGG CTGCCAAGGA GAACGTGGTC 2040

CTGGAGGTCA CAGTCCTGAA CACAGAGGGC CAGGTGCAGG AGCTGGTGTT CCCCCAGGAG 2100

109

GAGTACCCGA GAAAGAACTC CATCCAGCTG TCTGCCAAAA CCATCAAGCA GAACAGCCGC 2160

AATGGGGTGG TCAAAGTTGT CTTCATCCTC TACAACAACC TGGGCCTCTT CCTGTCCACG 2220

GAGAATGCCA CAGTGAAGCT GGCCGGCGAA GCAGGCCCGG GTGGCCCTGG GGGCGCCTCT 2280

CTAGTGGTGA ACTCACAGGT CATCGCAGCA TCCATCAACA AGGAGTCCAG CCGCGTCTTC 2340

CTCATGGACC CTGTCATCTT CACCGTGGCC CACCTGGAGG ACAAGAACCA CTTCAATGCT 2400

AACTGCTCCT TCTGGAACTA CTCGGAGCGT TCCATGCTGG GCTATTGGTC GACCCAAGGC 2460

TGCCGCCTGG TGGAGTCCAA CAAGACCCAT ACCACGTGTG CCTGCAGCCA CCTCACCAAC 2520

TTCGCTGTGC TCATGGCTCA CCGTGAGATC TACCAGGGCC GCATCAACGA GCTGCTGCTG 2580

TCGGTCATCA CCTGGGTGGG CATTGTGATC TCCCTGGTCT GCTTGGCCAT CTGCATCTCC 2640

ACCTTCTGCT TCCTGCGGGG GCTGCAGACC GACCGCAACA CCATCCACAA GAACCTGTGC 2700

ATCAACCTCT TCCTGGCTGA GCTGCTCTTC CTGGTCGGGA TCGACAAGAC TCAGTATGAG 2760

ATTGCCTGCC CCATCTTCGC CGGCCTGCTG CACTATTTCT TCCTGGCTGC CTTCTCCTGG 2820

CTGTGCCTGG AGGGCGTGCA CCTCTACCTG CTACTAGTGG AGGTGTTTGA GAGCGAGTAT 2880

TCCCGCACCA AGTACTACTA CCTGGGTGGC TACTGCTTCC CGGCCCTGGT GGTGGGCATC 2940

GCGGCTGCCA TTGACTACCG CAGCTACGGC ACCGAGAAGG CCTGCTGGCT CCGAGTGGAC 3000

AATTACTTCA TCTGGAGTTT CATCGGGCCA GTCTCCTTCG TTATCGTGGT CAACCTGGTG 3060

TTCCTCATGG TGACCCTGCA CAAGATGATC CGAAGCTCAT CTGTGCTCAA GCCCGACTCC 3120

AGCCGCCTGG ACAACATTAA ATCCTGGGCG CTGGGGGCCA TCGCGCTGCT GTTCCTGCTG 3180

GGCCTCACCT GGGCTTTCGG CCTCCTCTTC ATCAACAAGG AGTCGGTGGT CATGGCCTAT 3240

CTCTTCACCA CCTTCAACGC CTTCCAGGGG GTCTTCATCT TCGTCTTTCA CTGCGCCTTA 3300

CAGAAGAAGG TGCACAAGGA GTACAGCAAG TGCCTGCGTC ACTCCTACTG CTGCATCCGC 3360

TCCCCACCCG GGGGCACTCA CGGATCCCTC AAGACCTCAG CCATGCGAAG CAACACCCGC 3420

TACTACACAG GGACCCAGAG CCGAATTCGG AGGATGTGGA ATGACACTGT GAGGAAACAG 3480

ACGGAGTCCT CCTTCATGGC GGGTGACATC AACAGCACCC CCACCCTGAA CCGAGGTACC 3540

ATGGGGAACC ACCTGCTGAC CAACCCCGTG CTGCAGCCCC GTGGGGGCAC CAGTCCCTAC 3600

110

AACACCCTCA TCGCCGAGTC AGTGGGCTTC AATCCCTCCT CGCCCCCTGT CTTCAACTCC 3660

CCAGGGAGCT ACCGGGAACC CAAGCACCCC TTGGGAGGCC GGGAAGCCTG TGGCATGGAC 3720

ACCCTGCCCC TGAACGGCAA CTTCAATAAC AGTTACTCCT TGCGAAGTGG GGATTTCCCT 3780

CCCGGGGATG GGGGCCCTGA GCCGCCCCGA GGCCGGAACC TAGCCGATGC GGCGGCCTTT 3840

GAGAAGATGA TCATCTCAGA GCTGGTGCAC AACAACCTGC GGGGGAGCAG CAGCGCGGCC 3900

AAGGGCCCTC CACCGCCTGA GCCCCCTGTG CCACCTGTGC CAGGGGGCGG GGGCGAGGAA 3960

GAGGCGGGCG GGCCCGGGGG TGCTGACCGG GCCGAGATTG AACTTCTCTA TAAGGCCCTG 4020

GAGGAGCCTC TGCTGCTGCC CCGGGCCCAG TCGGTGCTGT ACCAGAGCGA TCTGGACGAG 4080

TCGGAGAGCT GCACGGCCGA GGACGGCGCC ACCAGCCGGC CCCTCTCCTC CCCTCCTGGC 4140

CGGGACTCCC TCTATGCCAG CGGGGCCAAC CTGCGGGACT CACCCTCCTA CCCGGACAGC 4200

AGCCCTGAGG GGCCCAGTGA GGCCCTGCCC CCACCCCCTC CCGCACCCCC CGGCCCCCCC 4260

GAAATCTACT ACACCTCGCG CCCGCCAGCC CTGGTGGCCC GGAATCCCCT GCAGGGCTAC 4320

TACCAGGTGC GGCGTCCTAG CCACGAGGGC TACCTGGCAG CCCCAGGCCT TGAGGGGCCA 4380

GGGCCCGATG GGGACGGGCA GATGCAGCTG GTCACCAGTC TC   4425

SEQUENCE LISTING

<110> Ohara, Osamu
<110> Nagase, Takahiro
<110> Nomura, Nobuo
<110> Hinuma, Shuji
<110> Fujii, Ryo
<110> Kitahara, Osamu
<110> Mogi, Shinichi
<120> Novel G Protein Coupled Receptor Protein and Its Use
<130> 2534US0P
<140>
<141>
<150> PCT/JP99/03909
<151> 1998-07-22
<150> JP 10-207579
<151> 1998-07-23
<150> JP 10-225060
<151> 1998-08-07
<150> JP 10-284328
<151> 1998-10-06
<160> 6
<170>

<210> 1
<211> 872
<212> PRT
<213> Human
<400> 1

```
Ala Glu Gln Thr Arg Asn His Leu Asn Ala Gly Asp Ile Thr Tyr Ser
 1               5                  10                  15
Val Arg Ala Met Asp Gln Leu Val Gly Leu Leu Asp Val Gln Leu Arg
                20                  25                  30
Asn Leu Thr Pro Gly Gly Lys Asp Ser Ala Ala Arg Ser Leu Asn Lys
            35                  40                  45
Ala Met Val Glu Thr Val Asn Asn Leu Leu Gln Pro Gln Ala Leu Asn
        50                  55                  60
Ala Trp Arg Asp Leu Thr Thr Ser Asp Gln Leu Arg Ala Ala Thr Met
 65                  70                  75                  80
Leu Leu His Thr Val Glu Glu Ser Ala Phe Val Leu Ala Asp Asn Leu
                85                  90                  95
Leu Lys Thr Asp Ile Val Arg Glu Asn Thr Asp Asn Ile Lys Leu Glu
                100                 105                 110
Val Ala Arg Leu Ser Thr Glu Gly Asn Leu Glu Asp Leu Lys Phe Pro
            115                 120                 125
Glu Asn Met Gly His Gly Ser Thr Ile Gln Leu Ser Ala Asn Thr Leu
        130                 135                 140
Lys Gln Asn Gly Arg Asn Gly Glu Ile Arg Val Ala Phe Val Leu Tyr
145                 150                 155                 160
Asn Asn Leu Gly Pro Tyr Leu Ser Thr Glu Asn Ala Ser Met Lys Leu
                165                 170                 175
Gly Thr Glu Ala Leu Ser Thr Asn His Ser Val Ile Val Asn Ser Pro
            180                 185                 190
Val Ile Thr Ala Ala Ile Asn Lys Glu Phe Ser Asn Lys Val Tyr Leu
            195                 200                 205
Ala Asp Pro Val Val Phe Thr Val Lys His Ile Lys Gln Ser Glu Glu
        210                 215                 220
Asn Phe Asn Pro Asn Cys Ser Phe Trp Ser Tyr Ser Lys Arg Thr Met
225                 230                 235                 240
Thr Gly Tyr Trp Ser Thr Gln Gly Cys Arg Leu Leu Thr Thr Asn Lys
                245                 250                 255
Thr His Thr Thr Cys Ser Cys Asn His Leu Thr Asn Phe Ala Val Leu
            260                 265                 270
Met Ala His Val Glu Val Lys His Ser Asp Ala Val His Asp Leu Leu
        275                 280                 285
Leu Asp Val Ile Thr Trp Val Gly Ile Leu Leu Ser Leu Val Cys Leu
```

```
          290                     295                     300
Leu Ile Cys Ile Phe Thr Phe Cys Phe Phe Arg Gly Leu Gln Ser Asp
305                     310                     315                     320
Arg Asn Thr Ile His Lys Asn Leu Cys Ile Ser Leu Phe Val Ala Glu
                325                     330                     335
Leu Leu Phe Leu Ile Gly Ile Asn Arg Thr Asp Gln Pro Ile Ala Cys
                340                     345                     350
Ala Val Phe Ala Ala Leu Leu His Phe Phe Phe Leu Ala Ala Phe Thr
                355                     360                     365
Trp Met Phe Leu Glu Gly Val Gln Leu Tyr Ile Met Leu Val Glu Val
                370                     375                     380
Phe Glu Ser Glu His Ser Arg Arg Lys Tyr Phe Tyr Leu Val Gly Tyr
385                     390                     395                     400
Gly Met Pro Ala Leu Ile Val Ala Val Ser Ala Ala Val Asp Tyr Arg
                405                     410                     415
Ser Tyr Gly Thr Asp Lys Val Cys Trp Leu Arg Leu Asp Thr Tyr Phe
                420                     425                     430
Ile Trp Ser Phe Ile Gly Pro Ala Thr Leu Ile Ile Met Leu Asn Val
                435                     440                     445
Ile Phe Leu Gly Ile Ala Leu Tyr Lys Met Phe His His Thr Ala Ile
                450                     455                     460
Leu Lys Pro Glu Ser Gly Cys Leu Asp Asn Ile Lys Ser Trp Val Ile
465                     470                     475                     480
Gly Ala Ile Ala Leu Leu Cys Leu Leu Gly Leu Thr Trp Ala Phe Gly
                485                     490                     495
Leu Met Tyr Ile Asn Glu Ser Thr Val Ile Met Ala Tyr Leu Phe Thr
                500                     505                     510
Ile Phe Asn Ser Leu Gln Gly Met Phe Ile Phe Ile Phe His Cys Val
                515                     520                     525
Leu Gln Lys Lys Val Arg Lys Glu Tyr Gly Lys Cys Leu Arg Thr His
                530                     535                     540
Cys Cys Ser Gly Lys Ser Thr Glu Ser Ser Ile Gly Ser Gly Lys Thr
545                     550                     555                     560
Ser Gly Ser Arg Thr Pro Gly Arg Tyr Ser Thr Gly Ser Gln Ser Arg
                565                     570                     575
Ile Arg Arg Met Trp Asn Asp Thr Val Arg Lys Gln Ser Glu Ser Ser
                580                     585                     590
Phe Ile Thr Gly Asp Ile Asn Ser Ser Ala Ser Leu Asn Arg Glu Gly
                595                     600                     605
Leu Leu Asn Asn Ala Arg Asp Thr Ser Val Met Asp Thr Leu Pro Leu
                610                     615                     620
Asn Gly Asn His Gly Asn Ser Tyr Ser Ile Ala Ser Gly Glu Tyr Leu
625                     630                     635                     640
Ser Asn Cys Val Gln Ile Ile Asp Arg Gly Tyr Asn His Asn Glu Thr
                645                     650                     655
Ala Leu Glu Lys Lys Ile Leu Lys Glu Leu Thr Ser Asn Tyr Ile Pro
                660                     665                     670
Ser Tyr Leu Asn Asn His Glu Arg Ser Ser Glu Gln Asn Arg Asn Leu
                675                     680                     685
Met Asn Lys Leu Val Asn Asn Leu Gly Ser Gly Arg Glu Asp Asp Ala
                690                     695                     700
Ile Val Leu Asp Asp Ala Thr Ser Phe Asn His Glu Glu Ser Leu Gly
705                     710                     715                     720
Leu Glu Leu Ile His Glu Glu Ser Asp Ala Pro Leu Leu Pro Pro Arg
                725                     730                     735
Val Tyr Ser Thr Glu Asn His Gln Pro His His Tyr Thr Arg Arg Arg
                740                     745                     750
Ile Pro Gln Asp His Ser Glu Ser Phe Phe Pro Leu Leu Thr Asn Glu
                755                     760                     765
His Thr Glu Asp Leu Gln Ser Pro His Arg Asp Ser Leu Tyr Thr Ser
                770                     775                     780
Met Pro Thr Leu Ala Gly Val Ala Ala Thr Glu Ser Val Thr Thr Ser
785                     790                     795                     800
Thr Gln Thr Glu Pro Pro Pro Ala Lys Cys Gly Asp Ala Glu Asp Val
                805                     810                     815
Tyr Tyr Lys Ser Met Pro Asn Leu Gly Ser Arg Asn His Val His Gln
                820                     825                     830
```

Page 2

Leu His Thr Tyr Tyr Gln Leu Gly Arg Gly Ser Ser Asp Gly Phe Ile
        835   840   845
Val Pro Pro Asn Lys Asp Gly Thr Pro Pro Glu Gly Ser Ser Lys Gly
    850   855   860
Pro Ala His Leu Val Thr Ser Leu
865   870

<210> 2
<211> 2616
<212> DNA
<213> Human
<400> 2

GCTGAACAGA CAAGAAATCA CTTGAATGCT GGGGACATCA CCTACTCTGT CCGGGCCATG 60
GACCAGCTGG TAGGCCTCCT AGATGTACAG CTTCGGAACT TGACCCCAGG TGGAAAAGAT 120
AGTGCTGCCC GGAGTTTGAA CAAGGCAATG GTCGAGACAG TTAACAACCT CCTTCAGCCA 180
CAAGCTTTGA ATGCATGGAG AGACCTGACT ACGAGTGATC AGCTGCGTGC GGCCACCATG 240
TTGCTTCATA CTGTGGAGGA AAGTGCTTTT GTGCTGGCTG ATAACCTTTT GAAGACTGAC 300
ATTGTCAGGG AGAATACAGA CAATATTAAA TTGGAAGTTG CAAGACTGAG CACAGAAGGA 360
AACTTAGAAG ACCTAAAATT TCCAGAAAAC ATGGGCCATG GAAGCACTAT CCAGCTGTCT 420
GCAAATACCT TAAAGCAAAA TGGCCGAAAT GGAGAGATCA GAGTGGCCTT TGTCCTGTAT 480
AACAACTTGG GTCCTTATTT ATCCACGGAG AATGCCAGTA TGAAGTTGGG AACGGAAGCT 540
TTGTCCACAA ATCATTCTGT TATTGTCAAT TCCCCTGTTA TTACGGCAGC AATAAACAAA 600
GAGTTCAGTA CAAGGTTTA TTTGGCTGAT CCTGTGGTAT TTACTGTTAA ACATATCAAG 660
CAGTCAGAGG AAAATTTCAA CCCTAACTGT TCATTTTGGA GCTACTCCAA GCGTACAATG 720
ACAGGTTATT GGTCAACACA AGGCTGTCGG CTCCTGACAA CAAATAAGAC ACATACTACA 780
TGCTCTTGTA ACCACCTAAC AAATTTTGCA GTACTGATGG CACATGTGGA AGTTAAGCAC 840
AGTGATGCGG TCCATGACCT CCTTCTGGAT GTGATCACGT GGGTTGGAAT TTTGCTGTCC 900
CTTGTTTGTC TCCTGATTTG CATCTTCACA TTTTTGCTTT TCCGCGGGCT CCAGAGTGAC 960
CGTAACACCA TCCACAAGAA CCTCTGCATC AGTCTCTTTG TAGCAGAGCT GCTCTTCCTG 1020
ATTGGGATCA ACCGAACTGA CCAACCAATT GCCTGTGCTG TTTTCGCTGC CCTGTTTTCT 1080
TCTTCTTGGC TGCCTTCACC TGGATGTTCC TGGAGGGGGT GCAGCTTTAT ATACATCATG 1140
CTGGTGGAGG TTTTTGAGAG TGAACATTCA CGTAGGAAAT ACTTTTATCT GGTCGGCTAT 1200
GGGATGCCTG CACTCATTGT GGCTGTGTCA GCTGCAGTAG ACTACAGGAG TTATGGAACA 1260
GATAAAGTAT GTTGGCTCCG ACTTGACACC TACTTCATTT GGAGTTTTAT AGGACCAGCA 1320
ACTTTGATAA TTATGCTTAA TGTAATCTTC CTTGGGATTG CTTTATATAA AATGTTTCAT 1380
CATACTGCTA TACTGAAACC TGAATCAGGC TGTCTTGATA ACATCAAGTC ATGGGTTATA 1440
GGTGCAATAG CTCTTCTCTG CCTATTAGGA TTGACCTGGG CCTTTGGACT CATGTATATT 1500
AATGAAAGCA CAGTCATCAT GGCCTATCTC TTCACCATTT TCAATTCTCT CACAGGGAATG 1560
TTTATATTTA TTTTCCATTG TGTCCTACAG AAGAAGGTAC GAAAAGGTAT TGGGGAAATGC 1620
CTGCGAACAC ATTGCTGTAG TGGCAAAAGT ACAGAGAGTT CCATTGGTTC AGGGAAAACA 1680
TCTGGTTCTC GAACTCCTGG ACGCTACTCC ACAGGCTCAC AGAGCCGAAT CCGTAGAATG 1740
TGGAATGACA CGGTTCGAAA GCAGTCAGAG TCTTCCTTTA TTACTGGAGA CATAAACAGT 1800
TCAGCGTCAC TCAACAGAGA GGGGCTTCTG AACAATGCCA GGGATACAAG TGTCATGGAT 1860
ACTCTACCAC TGAATGGTAA CCATGGCAAT AGTTACAGCA TTGCCAGCGG CGAATACCTG 1920
AGCAACTGTG TGCAAATCAT AGACCGTGGC TATAACCATA ACGAGACCGC CCTAGAGAAA 1980
AAGATTCTGA AGGAACTCAC TTCCAACTAT ATCCCTTCTT ACCTGAACAA CCATGAGCGC 2040
TCCAGTGAAC AGAACAGGAA TCTGATGAAC AAGCTGGTGA ATAACCTTGG CAGTGGAAGG 2100
GAAGATGATG CCATTGTCCT GGATGATGCC ACCTCGTTTA ACCACGAGGA GAGTTTGGGC 2160
CTGGAACTCA TTCATGAGGA ATCTGATGCT CCTTTGCTGC CCCCAAGAGT ATACTCCACC 2220
GAGAACCACC AGCCACACCA TTATACCAGA AGGCGGATCC CCCAAGACCA CAGTGAGAGC 2280
TTTTTCCCTT TGCTAACCAA CGAGCACACA GAAGATCTCC AGTCACCCCA TAGAGACTCT 2340
CTCTATACCA GCATGCCGAC ACTGGCTGGT GTGGCCGCCA CAGAGAGTGT TACCACCAGC 2400
ACCCAGACCG AACCCCCACC GGCCAAATGT GGTGATGCCG AAGATGTTTA CTACAAAAGC 2460
ATGCCAAACC TAGGCTCCAG AAACCACGTC CATCAGCTGC ATACTTACTA CCAGCTAGGT 2520
CGCGGCAGCA GTGATGGATT TATAGTTCCT CCAAACAAAG ATGGGACCCC TCCCGAGGGA 2580
AGTTCAAAAG GACCGGCTCA TTTGGTCACT AGTCTA 2616

<210> 3
<211> 1021
<212> PRT
<213> Human
<400> 3

Glu Gly Ser Lys Gly Thr Lys Pro Pro Pro Ala Val Ser Thr Thr Lys
 1   · 5   10   15
Ile Pro Pro Ile Thr Asn Ile Phe Pro Leu Pro Glu Arg Phe Cys Glu

```
                20                      25                      30
Ala Leu Asp Ser Lys Gly Ile Lys Trp Pro Gln Thr Gln Arg Gly Met
              35                      40                      45
Met Val Glu Arg Pro Cys Pro Lys Gly Thr Arg Gly Thr Ala Ser Tyr
          50                      55                      60
Leu Cys Met Ile Ser Thr Gly Thr Trp Asn Pro Lys Gly Pro Asp Leu
65                      70                      75                      80
Ser Asn Cys Thr Ser His Trp Val Asn Gln Leu Ala Gln Lys Ile Arg
                  85                      90                      95
Ser Gly Glu Asn Ala Ala Ser Leu Ala Asn Glu Leu Ala Lys His Thr
                  100                     105                     110
Lys Gly Pro Val Phe Ala Gly Asp Val Ser Ser Ser Val Arg Leu Met
          115                     120                     125
Glu Gln Leu Val Asp Ile Leu Asp Ala Gln Leu Gln Glu Leu Lys Pro
          130                     135                     140
Ser Glu Lys Asp Ser Ala Gly Arg Ser Tyr Asn Lys Leu Gln Lys Arg
145                     150                     155                     160
Glu Lys Thr Cys Arg Ala Tyr Leu Lys Ala Ile Val Asp Thr Val Asp
                  165                     170                     175
Asn Leu Leu Arg Pro Glu Ala Leu Glu Ser Trp Lys His Met Asn Ser
              180                     185                     190
Ser Glu Gln Ala His Thr Ala Thr Met Leu Leu Asp Thr Leu Glu Glu
              195                     200                     205
Gly Ala Phe Val Leu Ala Asp Asn Leu Leu Glu Pro Thr Arg Val Ser
          210                     215                     220
Met Pro Thr Glu Asn Ile Val Leu Glu Val Ala Val Leu Ser Thr Glu
225                     230                     235                     240
Gly Gln Ile Gln Asp Phe Lys Phe Pro Leu Gly Ile Lys Gly Ala Gly
              245                     250                     255
Ser Ser Ile Gln Leu Ser Ala Asn Thr Val Lys Gln Asn Ser Arg Asn
              260                     265                     270
Gly Leu Ala Lys Leu Val Phe Ile Ile Tyr Arg Ser Leu Gly Gln Phe
          275                     280                     285
Leu Ser Thr Glu Asn Ala Thr Ile Lys Leu Gly Ala Asp Phe Ile Gly
290                     295                     300
Arg Asn Ser Thr Ile Ala Val Asn Ser His Val Ile Ser Val Ser Ile
305                     310                     315                     320
Asn Lys Glu Ser Ser Arg Val Tyr Leu Thr Asp Pro Val Leu Phe Thr
                  325                     330                     335
Leu Pro His Ile Asp Pro Asp Asn Tyr Phe Asn Ala Asn Cys Ser Phe
              340                     345                     350
Trp Asn Tyr Ser Glu Arg Thr Met Met Gly Tyr Trp Ser Thr Gln Gly
          355                     360                     365
Cys Lys Leu Val Asp Thr Asn Lys Thr Arg Thr Thr Cys Ala Cys Ser
370                     375                     380
His Leu Thr Asn Phe Ala Ile Leu Met Ala His Arg Glu Ile Ala Tyr
385                     390                     395                     400
Lys Asp Gly Val His Glu Leu Leu Leu Thr Val Ile Thr Trp Val Gly
              405                     410                     415
Ile Val Ile Ser Leu Val Cys Leu Ala Ile Cys Ile Phe Thr Phe Cys
          420                     425                     430
Phe Phe Arg Gly Leu Gln Ser Asp Arg Asn Thr Ile His Lys Asn Leu
          435                     440                     445
Cys Ile Asn Leu Phe Ile Ala Glu Phe Ile Phe Leu Ile Gly Ile Asp
450                     455                     460
Lys Thr Lys Tyr Ala Ile Ala Cys Pro Ile Phe Ala Gly Leu Leu His
465                     470                     475                     480
Phe Phe Phe Leu Ala Ala Phe Ala Trp Met Cys Leu Glu Gly Val Gln
              485                     490                     495
Leu Tyr Leu Met Leu Val Glu Val Phe Glu Ser Glu Tyr Ser Arg Lys
          500                     505                     510
Lys Tyr Tyr Tyr Val Ala Gly Tyr Leu Phe Pro Ala Thr Val Val Gly
      515                     520                     525
Val Ser Ala Ala Ile Asp Tyr Lys Ser Tyr Gly Thr Glu Lys Ala Cys
530                     535                     540
Trp Leu His Val Asp Asn Tyr Phe Ile Trp Ser Phe Ile Gly Pro Val
545                     550                     555                     560
```

Page 4

```
Thr Phe Ile Ile Leu Leu Asn Ile Ile Phe Leu Val Ile Thr Leu Cys
            565                     570                 575
Lys Met Val Lys His Ser Asn Thr Leu Lys Pro Asp Ser Ser Arg Leu
            580                     585                 590
Glu Asn Ile Lys Ser Trp Val Leu Gly Ala Phe Ala Leu Leu Cys Leu
            595                     600                 605
Leu Gly Leu Thr Trp Ser Phe Gly Leu Leu Phe Ile Asn Glu Glu Thr
            610                 615                 620
Ile Val Met Ala Tyr Leu Phe Thr Ile Phe Asn Ala Phe Gln Gly Val
625                     630                 635                 640
Phe Ile Phe Ile Phe His Cys Ala Leu Gln Lys Lys Val Arg Lys Glu
                    645                 650                 655
Tyr Gly Lys Cys Phe Arg His Ser Tyr Cys Cys Gly Gly Leu Pro Thr
                660                 665                 670
Glu Ser Pro His Ser Ser Val Lys Ala Ser Thr Thr Arg Thr Ser Ala
        675                 680                 685
Arg Tyr Ser Ser Gly Thr Gln Ser Arg Ile Arg Arg Met Trp Asn Asp
        690                 695                 700
Thr Val Arg Lys Gln Ser Glu Ser Ser Phe Ile Ser Gly Asp Ile Asn
705                 710                 715                 720
Ser Thr Ser Thr Leu Asn Gln Gly Met Thr Gly Asn Tyr Leu Leu Thr
            725                 730                 735
Asn Pro Leu Leu Arg Pro His Gly Thr Asn Asn Pro Tyr Asn Thr Leu
            740                 745                 750
Leu Ala Glu Thr Val Val Cys Asn Ala Pro Ser Ala Pro Val Phe Asn
        755                 760                 765
Ser Pro Gly His Ser Leu Asn Asn Ala Arg Asp Thr Ser Ala Met Asp
        770                 775                 780
Thr Leu Pro Leu Asn Gly Asn Phe Asn Asn Ser Tyr Ser Leu His Lys
785                 790                 795                 800
Gly Asp Tyr Asn Asp Ser Val Gln Val Val Asp Cys Gly Leu Ser Leu
            805                 810                 815
Asn Asp Thr Ala Phe Glu Lys Met Ile Ile Ser Glu Leu Val His Asn
            820                 825                 830
Asn Leu Arg Gly Ser Ser Lys Thr His Asn Leu Glu Leu Thr Leu Pro
        835                 840                 845
Val Lys Pro Val Ile Gly Gly Ser Ser Ser Glu Asp Asp Ala Ile Val
    850                 855                 860
Ala Asp Ala Ser Ser Leu Met His Ser Asp Asn Pro Gly Leu Glu Leu
865                 870                 875                 880
His His Lys Glu Leu Glu Ala Pro Leu Ile Pro Gln Arg Thr His Ser
            885                 890                 895
Leu Leu Tyr Gln Pro Gln Lys Lys Val Lys Ser Glu Gly Thr Asp Ser
        900                 905                 910
Tyr Val Ser Gln Leu Thr Ala Glu Ala Glu Asp His Leu Gln Ser Pro
    915                 920                 925
Asn Arg Asp Ser Leu Tyr Thr Ser Met Pro Asn Leu Arg Asp Ser Pro
    930                 935                 940
Tyr Pro Glu Ser Ser Pro Asp Met Glu Glu Asp Leu Ser Pro Ser Arg
945                 950                 955                 960
Arg Ser Glu Asn Glu Asp Ile Tyr Tyr Lys Ser Met Pro Asn Leu Gly
            965                 970                 975
Ala Gly His Gln Leu Gln Met Cys Tyr Gln Ile Ser Arg Gly Asn Ser
        980                 985                 990
Asp Gly Tyr Ile Ile Pro Ile Asn Lys Glu Gly Cys Ile Pro Glu Gly
    995                 1000                1005
Asp Val Arg Glu Gly Gln Met Gln Leu Val Thr Ser Leu
    1010                1015                1020
```

<210> 4
<211> 3063
<212> DNA
<213> Human
<400> 4

```
GAAGGAAGCA AAGGGACAAA ACCACCTCCA GCAGTTTCTA CAACCAAAAT TCCACCTATA    60
ACAAATATTT TTCCCCTGCC AGAGAGATTC TGTGAAGCAT TAGACTCCAA GGGGATAAAG   120
```

```
TGGCCTCAGA CACAAAGGGG AATGATGGTT GAACGACCAT GCCCTAAGGG AACAAGAGGA   180
ACTGCCTCAT ATCTCTGCAT GATTTCCACT GGAACATGGA ACCCTAAGGG CCCCGATCTT   240
AGCAACTGTA CCTCACACTG GGTGAATCAG CTGGCTCAGA AGATCAGAAG CGGAGAAAAT   300
GCTGCTAGTC TTGCCAATGA ACTGGCTAAA CATACCAAAG GGCCAGTGTT TGCTGGGGAT   360
GTAAGTTCTT CAGTGAGATT GATGGAGCAG TTGGTGGACA TCCTTGATGC ACAGCTGCAG   420
GAACTGAAAC CTAGTGAAAA AGATTCAGCT GGACGGAGTT ATAACAAGCT CCAAAAACGA   480
GAGAAGACAT GCAGGGCTTA CCTTAAGGCA ATTGTTGACA CAGTGGACAA CCTTCTGAGA   540
CCTGAAGCTT TGGAATCATG GAAACATATG AATTCTTCTG AACAAGCACA TACTGCAACA   600
ATGTTACTCG ATACATTGGA AGAAGGAGCT TTTGTCCTAG CTGACAATCT TTTAGAACCA   660
ACAAGGGTCT CAATGCCCAC AGAAAATATT GTCCTGGAAG TTGCCGTACT CAGTACAGAA   720
GGACAGATCC AAGACTTTAA ATTTCCTCTG GGCATCAAAG GAGCAGGCAG CTCAATCCAA   780
CTGTCCGCAA ATACCGTCAA ACAGAACAGC AGGAATGGGC TTGCAAAGTT GGTGTTCATC   840
ATTTACCGGA GCCTGGGACA GTTCCTTAGT ACAGAAAATG CAACCATTAA ACTGGGTGCT   900
GATTTTATTG GTCGTAATAG CACCATTGCA GTGAACTCTC ACGTCATTTC AGTTTCAATC   960
AATAAAGAGT CCAGCCGAGT ATACCTGACT GATCCTGTGC TTTTTACCCT GCCACACATT  1020
GATCCTGACA ATTATTTCAA TGCAAACTGC TCCTTCTGGA ACTACTCAGA GAGAACTATG  1080
ATGGGATATT GGTCTACCCA GGGCTGCAAG CTGGTTGACA CTAATAAAAC TCGAACAACG  1140
TGTGCATGCA GCCACCTAAC CAATTTTGCA ATTCTCATGG CCCACAGGGA AATTGCATAT  1200
AAAGATGGCG TTCATGAATT ACTTCTTACA GTCATCACCT GGGTGGGAAT TGTCATTTCC  1260
CTTGTTTGCC TGGCTATCTG CATCTTCACC TTCTGCTTTT TCCGTGGCCT ACAGAGTGAC  1320
CGAAATACTA TTCACAAGAA CCTTTGTATC AACCTTTTCA TTGCTGAATT TATTTTCCTA  1380
ATAGGCATTG ATAAGACAAA ATATGCGATT GCATGCCCAA TATTTGCAGG ACTTCTACAC  1440
TTTTTCTTTT TGGCAGCTTT TGCTTGGATG TGCCTAGAAG GTGTGCAGCT CTACCTAATG  1500
TTAGTTGAAG TTTTTGAAAG TGAATATTCA AGGAAAAAAT ATTACTATGT TGCTGGTTAC  1560
TTGTTTCCTG CCACAGTGGT TGGAGTTTCA GCTGCTATTG ACTATAAGAG CTATGGAACA  1620
GAAAAAGCTT GCTGGCTTCA TGTTGATAAC TACTTTATAT GGAGCTTCAT TGGACCTGTT  1680
ACCTTCATTA TTCTGCTAAA TATTATCTTC TTGGTGATCA CATTGTGCAA AATGGTGAAG  1740
CATTCAAACA CTTTGAAACC AGATTCTAGC AGGTTGGAAA ACATTAAGTC TTGGGTGCTT  1800
GGCGCTTTCG CTCTTCTGTG TCTTCTTGGC CTCACCTGGT CCTTTGGGTT GCTTTTTATT  1860
AATGAGGAGA CTATTGTGAT GGCATATCTC TTCACTATAT TTAATGCTTT CCAGGGAGTG  1920
TTCATTTTCA TCTTTCACTG TGCTCTCCAA AAGAAAGTAC GAAAAGAATA TGGCAAGTGC  1980
TTCAGACACT CATACTGCTG TGGAGGCCTC CCAACTGAGA GTCCCCACAG TTCAGTGAAG  2040
GCATCAACCA CCAGAACCAG TGCTCGCTAT TCCTCTGGCA CACAGAGTCG TATAAGAAGA  2100
ATGTGGAATG ATACTGTGAG AAAACAATCA GAATCTTCTT TTATCTCAGG TGACATCAAT  2160
AGCACTTCAA CACTTAATCA AGGAATGACT GGCAATTACC TACTAACAAA CCCTCTTCTT  2220
CGACCCCACG GCACTAACAA CCCCTATAAC ACATTGCTCG CTGAAACAGT TGTATGTAAT  2280
GCCCCTTCAG CTCCTGTATT TAACTCACCA GGACATTCAC TGAACAATGC CAGGGATACA  2340
AGTGCCATGG ATACTCTACC GCTAAATGGT AATTTTAACA ACAGCTACTC GCTGCACAAG  2400
GGTGACTATA ATGACAGCGT GCAAGTTGTG GACTGTGGAC TAAGTCTGAA TGATACTGCT  2460
TTTGAGAAAA TGATCATTTC AGAATTAGTG CACAACAACT TACGGGGCAG CAGCAAGACT  2520
CACAACCTCG AGCTCACGCT ACCAGTCAAA CCTGTGATTG GAGGTAGCAG CAGTGAAGAT  2580
GATGCTATTG TGGCAGATGC TTCATCTTTA ATGCACAGCG ACAACCCAGG GCTGGAGCTC  2640
CATCACAAAG AACTCGAGGC ACCACTTATT CCTCAGCGGA CTCACTCCCT TCTGTACCAA  2700
CCCCAGAAGA AGTGAAGTC CGAGGGAACT GACAGCTATG TCTCCCAACT GACAGCAGAG  2760
GCTGAAGATC ACCTACAGTC CCCCAACAGA GACTCTCTTT ATACAAGCAT GCCCAATCTT  2820
AGAGACTCTC CCTATCCGGA GAGCAGCCCT GACATGGAAG AAGACCTCTC TCCCTCCAGG  2880
AGGAGTGAGA ATGAGGACAT TTACTATAAA AGCATGCCAA ATCTTGGAGC TGGCCATCAG  2940
CTTCAGATGT GCTACCAGAT CAGCAGGGGC AATAGTGATG GTTATATAAT CCCCATTAAC  3000
AAAGAAGGGT GTATTCCAGA AGGAGATGTT AGAGAAGGAC AAATGCAGCT GGTTACAAG   3060
CTT                                                                3063

<210> 5
<211> 1474
<212> PRT
<213> Human

<400> 5

Met Ala Arg Leu Ala Ala Val Leu Trp Asn Leu Cys Val Thr Ala Val
                5                  10                  15
Leu Val Thr Ser Ala Thr Gln Gly Leu Ser Arg Ala Gly Leu Pro Phe
                20                 25                  30
Gly Leu Met Arg Arg Glu Leu Ala Cys Glu Gly Tyr Pro Ile Glu Leu
            35                 40                  45
Arg Cys Pro Gly Ser Asp Val Ile Met Val Glu Asn Ala Asn Tyr Gly
    50                 55                  60
Arg Thr Asp Asp Lys Ile Cys Asp Ala Asp Pro Phe Gln Met Glu Asn
  65                 70                  75                  80
```

Page 6

```
Val Gln Cys Tyr Leu Pro Asp Ala Phe Lys Ile Met Ser Gln Arg Cys
              85                      90                      95
Asn Asn Arg Thr Gln Cys Val Val Val Ala Gly Ser Asp Ala Phe Pro
            100                 105                 110
Asp Pro Cys Pro Gly Thr Tyr Lys Tyr Leu Glu Val Gln Tyr Asp Cys
            115                 120                 125
Val Pro Tyr Lys Val Glu Gln Lys Val Phe Val Cys Pro Gly Thr Leu
    130                 135                 140
Gln Lys Val Leu Glu Pro Thr Ser Thr His Glu Ser Glu His Gln Ser
145                 150                 155                 160
Gly Ala Trp Cys Lys Asp Pro Leu Gln Ala Gly Asp Arg Ile Tyr Val
                165                 170                 175
Met Pro Trp Ile Pro Tyr Arg Thr Asp Thr Leu Thr Glu Tyr Ala Ser
            180                 185                 190
Trp Glu Asp Tyr Val Ala Ala Arg His Thr Thr Thr Tyr Arg Leu Pro
        195                 200                 205
Asn Arg Val Asp Gly Thr Gly Phe Val Val Tyr Asp Gly Ala Val Phe
    210                 215                 220
Tyr Asn Lys Glu Arg Thr Arg Asn Ile Val Lys Tyr Asp Leu Arg Thr
225                 230                 235                 240
Arg Ile Lys Ser Gly Glu Thr Val Ile Asn Thr Ala Asn Tyr His Asp
                245                 250                 255
Thr Ser Pro Tyr Arg Trp Gly Gly Lys Thr Asp Ile Asp Leu Ala Val
            260                 265                 270
Asp Glu Asn Gly Leu Trp Val Ile Tyr Ala Thr Glu Gly Asn Asn Gly
        275                 280                 285
Arg Leu Val Val Ser Gln Leu Asn Pro Tyr Thr Leu Arg Phe Glu Gly
    290                 295                 300
Thr Trp Glu Thr Gly Tyr Asp Lys Arg Ser Ala Ser Asn Ala Phe Met
305                 310                 315                 320
Val Cys Gly Val Leu Tyr Val Leu Arg Ser Tyr Val Asp Asp Asp
                325                 330                 335
Ser Glu Ala Ala Gly Asn Arg Val Asp Tyr Ala Phe Asn Thr Asn Ala
            340                 345                 350
Asn Arg Glu Glu Pro Val Ser Leu Thr Phe Pro Asn Pro Tyr Gln Phe
            355                 360                 365
Ile Ser Ser Val Asp Tyr Asn Pro Arg Asp Asn Gln Leu Tyr Val Trp
    370                 375                 380
Asn Asn Tyr Phe Val Val Arg Tyr Ser Leu Glu Phe Gly Pro Pro Asp
385                 390                 395                 400
Pro Ser Ala Gly Pro Ala Thr Ser Pro Pro Leu Ser Thr Thr Thr Thr
                405                 410                 415
Ala Arg Pro Thr Pro Leu Thr Ser Thr Ala Ser Pro Ala Ala Thr Thr
            420                 425                 430
Pro Leu Arg Arg Ala Pro Leu Thr Thr His Pro Val Gly Ala Ile Asn
        435                 440                 445
Gln Leu Gly Pro Asp Leu Pro Pro Ala Thr Ala Pro Val Pro Ser Thr
    450                 455                 460
Arg Arg Pro Pro Ala Pro Asn Leu His Val Ser Pro Glu Leu Phe Cys
465                 470                 475                 480
Glu Pro Arg Glu Val Arg Arg Val Gln Trp Pro Ala Thr Gln Gln Gly
            485                 490                 495
Met Leu Val Glu Arg Pro Cys Pro Lys Gly Thr Arg Gly Ile Ala Ser
            500                 505                 510
Phe Gln Cys Leu Pro Ala Leu Gly Leu Trp Asn Pro Arg Gly Pro Asp
        515                 520                 525
Leu Ser Asn Cys Thr Ser Pro Trp Val Asn Gln Val Ala Gln Lys Ile
    530                 535                 540
Lys Ser Gly Glu Asn Ala Ala Asn Ile Ala Ser Glu Leu Ala Arg His
545                 550                 555                 560
Thr Arg Gly Ser Ile Tyr Ala Gly Asp Val Ser Ser Ser Val Lys Leu
                565                 570                 575
Met Glu Gln Leu Leu Asp Ile Leu Asp Ala Gln Leu Gln Ala Leu Arg
            580                 585                 590
Pro Ile Glu Arg Glu Ser Ala Gly Lys Asn Tyr Asn Lys Met His Lys
            595                 600                 605
Arg Glu Arg Thr Cys Lys Asp Tyr Ile Lys Ala Val Val Glu Thr Val
```

```
              610                     615                     620
Asp Asn Leu Leu Arg Pro Glu Ala Leu Glu Ser Trp Lys Asp Met Asn
625                     630                     635                     640
Ala Thr Glu Gln Val His Thr Ala Thr Met Leu Leu Asp Val Leu Glu
                        645                     650                     655
Glu Gly Ala Phe Leu Leu Ala Asp Asn Val Arg Glu Pro Ala Arg Phe
                        660                     665                     670
Leu Ala Ala Lys Glu Asn Val Val Leu Glu Val Thr Val Leu Asn Thr
                        675                     680                     685
Glu Gly Gln Val Gln Glu Leu Val Phe Pro Gln Glu Glu Tyr Pro Arg
                        690                     695                     700
Lys Asn Ser Ile Gln Leu Ser Ala Lys Thr Ile Lys Gln Asn Ser Arg
705                     710                     715                     720
Asn Gly Val Val Lys Val Val Phe Ile Leu Tyr Asn Asn Leu Gly Leu
                        725                     730                     735
Phe Leu Ser Thr Glu Asn Ala Thr Val Lys Leu Ala Gly Glu Ala Gly
                        740                     745                     750
Pro Gly Gly Pro Gly Gly Ala Ser Leu Val Val Asn Ser Gln Val Ile
                        755                     760                     765
Ala Ala Ser Ile Asn Lys Glu Ser Ser Arg Val Phe Leu Met Asp Pro
                        770                     775                     780
Val Ile Phe Thr Val Ala His Leu Glu Asp Lys Asn His Phe Asn Ala
785                     790                     795                     800
Asn Cys Ser Phe Trp Asn Tyr Ser Glu Arg Ser Met Leu Gly Tyr Trp
                        805                     810                     815
Ser Thr Gln Gly Cys Arg Leu Val Glu Ser Asn Lys Thr His Thr Thr
                        820                     825                     830
Cys Ala Cys Ser His Leu Thr Asn Phe Ala Val Leu Met Ala His Arg
                        835                     840                     845
Glu Ile Tyr Gln Gly Arg Ile Asn Glu Leu Leu Leu Ser Val Ile Thr
                        850                     855                     860
Trp Val Gly Ile Val Ile Ser Leu Val Cys Leu Ala Ile Cys Ile Ser
865                     870                     875                     880
Thr Phe Cys Phe Leu Arg Gly Leu Gln Thr Asp Arg Asn Thr Ile His
                        885                     890                     895
Lys Asn Leu Cys Ile Asn Leu Phe Leu Ala Glu Leu Leu Phe Leu Val
                        900                     905                     910
Gly Ile Asp Lys Thr Gln Tyr Glu Ile Ala Cys Pro Ile Phe Ala Gly
                        915                     920                     925
Leu Leu His Tyr Phe Phe Leu Ala Ala Phe Ser Trp Leu Cys Leu Glu
                        930                     935                     940
Gly Val His Leu Tyr Leu Leu Leu Val Glu Val Phe Glu Ser Glu Tyr
945                     950                     955                     960
Ser Arg Thr Lys Tyr Tyr Tyr Leu Gly Gly Tyr Cys Phe Pro Ala Leu
                        965                     970                     975
Val Val Gly Ile Ala Ala Ala Ile Asp Tyr Arg Ser Tyr Gly Thr Glu
                        980                     985                     990
Lys Ala Cys Trp Leu Arg Val Asp Asn Tyr Phe Ile Trp Ser Phe Ile
                        995                     1000                    1005
Gly Pro Val Ser Phe Val Ile Val Val Asn Leu Val Phe Leu Met Val
                        1010                    1015                    1020
Thr Leu His Lys Met Ile Arg Ser Ser Ser Val Leu Lys Pro Asp Ser
1025                    1030                    1035                    1040
Ser Arg Leu Asp Asn Ile Lys Ser Trp Ala Leu Gly Ala Ile Ala Leu
                        1045                    1050                    1055
Leu Phe Leu Leu Gly Leu Thr Trp Ala Phe Gly Leu Leu Phe Ile Asn
                        1060                    1065                    1070
Lys Glu Ser Val Val Met Ala Tyr Leu Phe Thr Thr Phe Asn Ala Phe
                        1075                    1080                    1085
Gln Gly Val Phe Ile Phe Val Phe His Cys Ala Leu Gln Lys Lys Val
                        1090                    1095                    1100
His Lys Glu Tyr Ser Lys Cys Leu Arg His Ser Tyr Cys Cys Ile Arg
1105                    1110                    1115                    1120
Ser Pro Pro Gly Gly Thr His Gly Ser Leu Lys Thr Ser Ala Met Arg
                        1125                    1130                    1135
Ser Asn Thr Arg Tyr Tyr Thr Gly Thr Gln Ser Arg Ile Arg Arg Met
                        1140                    1145                    1150
```

Page 8

```
Trp Asn Asp Thr Val Arg Lys Gln Thr Glu Ser Ser Phe Met Ala Gly
        1155                1160                1165
Asp Ile Asn Ser Thr Pro Thr Leu Asn Arg Gly Thr Met Gly Asn His
        1170                1175                1180
Leu Leu Thr Asn Pro Val Leu Gln Pro Arg Gly Gly Thr Ser Pro Tyr
1185                1190                1195                1200
Asn Thr Leu Ile Ala Glu Ser Val Gly Phe Asn Pro Ser Ser Pro Pro
                1205                1210                1215
Val Phe Asn Ser Pro Gly Ser Tyr Arg Glu Pro Lys His Pro Leu Gly
            1220                1225                1230
Gly Arg Glu Ala Cys Gly Met Asp Thr Leu Pro Leu Asn Gly Asn Phe
            1235                1240                1245
Asn Asn Ser Tyr Ser Leu Arg Ser Gly Asp Phe Pro Pro Gly Asp Gly
        1250                1255                1260
Gly Pro Glu Pro Pro Arg Gly Arg Asn Leu Ala Asp Ala Ala Ala Phe
1265                1270                1275                1280
Glu Lys Met Ile Ile Ser Glu Leu Val His Asn Asn Leu Arg Gly Ser
                1285                1290                1295
Ser Ser Ala Ala Lys Gly Pro Pro Pro Pro Glu Pro Pro Val Pro Pro
            1300                1305                1310
Val Pro Gly Gly Gly Gly Glu Glu Glu Ala Gly Gly Pro Gly Gly Ala
            1315                1320                1325
Asp Arg Ala Glu Ile Glu Leu Leu Tyr Lys Ala Leu Glu Glu Pro Leu
        1330                1335                1340
Leu Leu Pro Arg Ala Gln Ser Val Leu Tyr Gln Ser Asp Leu Asp Glu
1345                1350                1355                1360
Ser Glu Ser Cys Thr Ala Glu Asp Gly Ala Thr Ser Arg Pro Leu Ser
                1365                1370                1375
Ser Pro Pro Gly Arg Asp Ser Leu Tyr Ala Ser Gly Ala Asn Leu Arg
            1380                1385                1390
Asp Ser Pro Ser Tyr Pro Asp Ser Ser Pro Glu Gly Pro Ser Glu Ala
        1395                1400                1405
Leu Pro Pro Pro Pro Pro Ala Pro Pro Gly Pro Pro Glu Ile Tyr Tyr
        1410                1415                1420
Thr Ser Arg Pro Pro Ala Leu Val Ala Arg Asn Pro Leu Gln Gly Tyr
1425                1430                1435                1440
Tyr Gln Val Arg Arg Pro Ser His Glu Gly Tyr Leu Ala Ala Pro Gly
                1445                1450                1455
Leu Glu Gly Pro Gly Pro Asp Gly Asp Gly Gln Met Gln Leu Val Thr
            1460                1465                1470
Ser Leu
```

```
<210> 6
<211> 4422
<212> DNA
<213> Human
<400> 6
```

```
ATGGCCCGCC TAGCCGCAGT GCTCTGGAAT CTGTGTGTCA CCGCCGTCCT GGTCACCTCG 60
GCCACCCAAG GCCTGAGCCG GGCCGGGCTC CCGTTCGGGC TGATGCGCCG GGAGCTGGCG 120
TGTGAAGGCT ACCCCATCGA GCTGCGGTGC CCCGGCAGGC ACGTCATCAT GGTGGAGAAT 180
GCCAACTACG GGCGCACGGA CGACAAGATT TGCGATGCTG ACCCTTTCCA GATGGAGAAT 240
GTGCAGTGCT ACCTGCCGGA CGCCTTCAAG ATCATGTCAC AGAGGTGTAA CAACCGCACC 300
CAGTGCGTGG TGGTCGCCGG CTCGGATGCC TTTCCTGACC CCTGTCCTGG GACCTACAAG 360
TACCTGGAGG TGCAGTACGA CTGTGTCCCC TACAAAGTGG AGCAGAAAGT CTTCGTGTGC 420
CCAGGGACCC TGCAGAAGGT GCTGGAGCCC ACCTCGACAC ACGAGTCAGA GCACCAGTCT 480
GGCGCATGGT GCAAGGACCC GCTGCAGGCG GGTGACCGCA TCTACGTGAT GCCCTGGATC 540
CCCTACCGCA CGGACACACT GACTGAGTAT GCCTCGTGGG AGGACTACGT GGCCGCCCGC 600
CACACCACCA CCTACCGCCT GCCCAACCGC GTGGATGGCA CAGGCTTTGT GGTCTACGAT 660
GGTGCCGTCT TCTACAACAA GGAGCGCACG CGCAACATCG TCAAGTATGA CCTACGGACG 720
CGCATCAAGA GCGGGGAGAC GGTCATCAAT ACCGCCAACT ACCATGACAC CTCGCCCTAC 780
CGCTGGGGCG GAAAGACCGA CATTGACCTG GCGGTGGACG AGAACGGGCT GTGGGTCATC 840
TACGCCACTG AGGGCAACAA CGGGCGGCTG GTGGTGAGCC AGCTGAACCC CTACACACTG 900
CGCTTTGAGG GCACGTGGGA GACGGGTTAC GACAAGCGCT CGGCATCCAA CGCCTTCATG 960
GTGTGTGGGG TCCTGTACGT CCTGCGCTCC GTGTACGTGG ATGATGACAG CGAGGCGGCT 1020
GGCAACCGCG TGGACTATGC CTTCAACACC AATGCCAACC GCGAGGAGCC TGTCAGCCTC 1080
ACCTTCCCCA ACCCCTACCA GTTCATCTCC TCCGTTGACT ACAACCCTCG CGACAACCAG 1140
```

```
CTGTACGTCT GGAACAACTA TTTCGTGGTG CGCTACAGCC TGGAGTTCGG GCCGCCCGAC 1200
CCCAGTGCTG GCCCAGCCAC TTCCCCACCC CTCAGCACGA CCACCACAGC CAGGCCCACG 1260
CCCCTCACCA GCACAGCCTC GCCCGCAGCC ACCACCCCGC TCCGCCGGGC ACCCCTCACC 1320
ACGCACCCAG TGGGTGCCAT CAACCAGCTG GGACCTGATC TGCCTCCAGC CACAGCCCCA 1380
GTCCCCAGCA CCCGGCGGCC CCCAGCCCCG AATCTACACG TGTCCCCTGA GCTCTTCTGC 1440
GAGCCCCGAG AGGTACGGCG GGTCCAGTGG CCGGCCACCC AGCAGGGCAT GCTGGTGGAG 1500
AGGCCCTGCC CCAAGGGGAC TCGAGGAATT GCCTCCTTCC AGTGTCTACC AGCCTTGGGG 1560
CTCTGGAACC CCCGGGGCCC TGACCTCAGC AACTGCACCT CCCCCTGGGT CAACCAGGTG 1620
GCCCAGAAGA TCAAGAGTGG GGAGAACGCG GCCAACATCG CCAGCGAGCT GGCCCGACAC 1680
ACCCGGGGCT CCATCTACGC GGGGGACGTC TCCTCCTCTG TGAAGCTGAT GGAGCAGCTG 1740
CTGGACATCC TGGATGCCCA GCTGCAGGCC CTGCGGCCCA TCGAGCGCGA GTCAGCCGGC 1800
AAGAACTACA ACAAGATGCA CAAGCGAGAG AGAACTTGTA AGGATTATAT CAAGGCCGTG 1860
GTGGAGACAG TGGACAATCT GCTCCGGCCA GAAGCTCTGG AGTCCTGGAA GGACATGAAT 1920
GCCACGGAGC AGGTGCACAC GGCCACCATG CTCCTCGACG TCCTGGAGGA GGGCGCCTTC 1980
CTGCTGGCCG ACAATGTCAG GGAGCCTGCC CGCTTCCTGG CTGCCAAGGA GAACGTGGTC 2040
CTGGAGGTCA CAGTCCTGAA CACAGAGGGC CAGGTGCAGG AGCTGGTGTT CCCCCAGGAG 2100
GAGTACCCGA GAAAGAACTC CATCCAGCTG TCTGCCAAAA CCATCAAGCA GAACAGCCGC 2160
AATGGGGTGG TCAAAGTTGT CTTCATCCTC TACAACAACC TGGGCCTCTT CCTGTCCACG 2220
GAGAATGCCA CAGTGAAGCT GGCCGGCGAA GCAGGCCCGG GTGGCCCTGG GGGCGCCTCT 2280
CTAGTGGTGA ACTCACAGGT CATCGCAGCA TCCATCAACA AGGAGTCCAG CCGCGTCTTC 2340
CTCATGGACC CTGTCATCTT CACCGTGGCC CACCTGGAGG ACAAGAACCA CTTCAATGCT 2400
AACTGCTCCT TCTGGAACTA CTCGGAGCGT TCCATGCTGG GCTATTGGTC GACCCAAGGC 2460
TGCCGCCTGG TGGAGTCCAA CAAGACCCAT ACCACGTGTG CCTGCAGCCA CCTCACCAAC 2520
TTCGCTGTGC TCATGGCTCA CCGTGAGATC TACCAGGGCC GCATCAACGA GCTGCTGCTG 2580
TCGGTCATCA CCTGGGTGGG CATTGTGATC TCCCTGGTCT GCTTGGCCAT CTGCATCTCC 2640
ACCTTCTGCT TCCTGCGGGG GCTGCAGACC GACCGCAACA CCATCCACAA GAACCTGTGC 2700
ATCAACCTCT TCCTGGCTGA GCTGCTCTTC CTGGTCGGGA TCGACAAGAC TCAGTATGAG 2760
ATTGCCTGCC CCATCTTCGC CGGCCTGCTG CACTATTTCT TCCTGGCTGC CTTCTCCTGG 2820
CTGTGCCTGG AGGGCGTGCA CCTCTACCTG CTACTAGTGG AGGTGTTTGA GAGCGAGTAT 2880
TCCCGCACCA AGTACTACTA CCTGGGTGGC TACTGCTTCC CGGCCCCTGAA GGTGGGCATC 2940
GCGGCTGCCA TTGACTACCG CAGCTACGGC ACCGAGAAGG CCTGCTGGCT CCGAGTGGAC 3000
AATTACTTCA TCTGGAGTTT CATCGGGCCA GTCTCCTTCG TTATCGTGGT CAACCTGGTG 3060
TTCCTCATGG TGACCCTGCA CAAGATGATC CGAAGCTCAT CTGTGCTCAA GCCCGACTCC 3120
AGCCGCCTGG ACAACATTAA ATCCTGGGCG CTGGGGGCCA TCGCGCTGCT GTTCCTGCTG 3180
GGCCTCACCT GGGCTTTCGG CCTCCTCTTC ATCAACAAGG AGTCGGTGGT CATGGCCTAT 3240
CTCTTCACCA CCTTCAACGC CTTCCAGGGG GTCTTCATCT TCGTCTTTCA CTGCGCCTTA 3300
CAGAAGAAGG TGCACAAGGA GTACAGCAAG TGCCTGCGTC ACTCCTACTG CTGCATCCGC 3360
TCCCCACCCG GGGGCACTCA CGGATCCCTC AAGACCTCAG CCATGCGAAG CAACACCCGC 3420
TACTACACAG GGACCCAGAG CCGAATTCGG AGGATGTGGA ATGACACTGT GAGGAAACAG 3480
ACGGAGTCCT CCTTCATGGC GGGTGACATC AACAGCACCC CCACCCTGAA CCGAGGTACC 3540
ATGGGGAACC ACCTGCTGAC CAACCCCGTG CTGCAGCCCC GTGGGGGCAC CAGTCCCTAC 3600
AACACCCTCA TCGCCGAGTC AGTGGGCTTC AATCCCTCCT CGCCCCCTGT CTTCAACTCC 3660
CCAGGGAGCT ACCGGGAACC CAAGCACCCC TTGGGAGGCC GGGAAGCCTG TGGCATGGAC 3720
ACCCTGCCCC TGAACGGCAA CTTCAATAAC AGTTACTCCT TGCGAAGTGG GGATTTCCCT 3780
CCCGGGGATG GGGGCCCTGA GCCGCCCCGA GGCCGGAACC TAGCCGATGC GGCGGCCTTT 3840
GAGAAGATGA TCATCTCAGA GCTGGTGCAC AACAACCTGC GGGGGAGCAG CAGCGCGGCC 3900
AAGGGCCCTC CACCGCCTGA GCCCCCTGTG CCACCTGTGC CAGGGGGCGG GGGCGAGGAA 3960
GAGGCGGGCG GGCCCGGGGG TGCTGACCGG GCCGAGATTG AACTTCTCTA TAAGGCCCTG 4020
GAGGAGCCTC TGCTGCTGCC CCGGGCCCAG TCGGTGCTGT ACCAGAGCGA TCTGGACGAG 4080
TCGGAGAGCT GCACGCCCGA GGACGGCGCC ACCAGCCGGC CCCTCTCCTC CCCTGGACAGC 4140
CGGGACTCCC TCTATGCCAG CGGGGCCAAC CTGCGCGGACT CACCCTCCTA CCCGGACAGC 4200
AGCCCTGAGG GGCCCAGTGA GGCCCTGCCC CCACCCCCTC CCGCACCCCC CGGCCCCCCC 4260
GAAATCTACT ACACCTCGCG CCCGCCAGCC CTGGTGGCCC GGAATCCCCT GCAGGGCTAC 4320
TACCAGGTGC GGCGTCCTAG CCACGAGGGC TACCTGGCAG CCCCAGGCCT TGAGGGGCCA 4380
GGGCCCGATG GGGACGGGCA GATGCAGCTG GTCACCAGTC TC                 4425
```